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1 (bases 1 to 663)
De, B.E., Lahaye, A., Ledoux, P. and Detroz, R.
Xylanase, microorganisms for its production, DNA molecules, process
of preparation and use thereof
patent: EP 0698667-A 1 28-FEB-1996;
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Matches 663; Conservative 0; Mismatches 0; Indels
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PAT 20-APR-2002
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1 (bases 1 to 663)

S De, B.E. Lahaye, A. Ledoux, P. and Detroz, R.
Xylanase, microorganisms for its production, DNA molecules, process of preparation and use thereof

AL Patent: EP 0698667-A 2 28-FEB-1996;
SOLVAY (BE)
Other publication BE 1008751 960702
Other publication BR 9503454 960804
Other publication OF 953578 960127
Other publication FI 953578 960127
Other publication AC 2154628 960127
Other publication AC 2154628 960127
Other publication AC 2154628 960127
Other publication AC 2508655 960208.
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2 from Patent BP0698667
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                  1 (bases 1 to 663)
De Buyl, E., Lahaye, A., Ledoux, P. and Detroz, R.
Xylanase, microorganisms producing it, DNA molecules,
preparing this xylanase and uses of the latter
Patent: US 6346407-A 2 12-FEB-2002;
Location/Qualifiers
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ive 0; Mismatches 0;
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A48225
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1 (bases 1 to 663)
De Buyl,E., Lahaye,A., Ledoux,P. and Detroz,R.
Xylanase, microorganisms producing it, DNA molecules,
preparing this xylanase and uses of the latter
Patent: US 6346407-A 1 12-FEB-2002;
Location/Qualifiers
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Pred. No. 2.1e-169;
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Db 382 TGGGGCAACTGGCGACCCTAAGGGGACCATCACTTGATGGAGGA 441 Db 361 ACATATGATATCTACGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACA 420	RESULT 8 AR193052 LOCUS LOCUS LOCUS DEFINITION Sequence 5 from patent US 6346407. ACCESSION AR193052.1 GI:20239017 VERSION KEYWORDS SOURCE ORGANISM UNknown. Unclassified. REFERENCE 1 (bases 1 to 744) AUTHORS De BUYL, E., Labhaye, A., Ledoux, P. and Detroz, R. TITLE Xylanase, microorganisms producing it, DNA molecules, methods for preparing this xylanase and uses of the latter JOURNAL Patent: US 6346407-A 5 12-FEB-2002; FEATURES 1. 774 OCCURATION FAMILY CONTINES Location/Qualifiers	Query Match 100.0%; Score 663; DB 6; Length 744; Best Local Similarity 100.0%; Pred. No. 2.1e-169; Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Oy 1 CAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTTTTGGAAA 60	Qy 61 GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGG 120	121	181	241 TATTTATGCGTCTATGCACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGT [301 TGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGA
	RESULT 7 AR193051 AR193051 AR193051 AR193051 AR193051 ACCESSION AR193051 VERSION AR193051 UNCLASSION AR193051.1 GI:20239016 SOURCE UNCLASSION AR193051.1 GI:20239016 UNCLASSION UNCLASSICH		Oy 1 CAAATGGTCACGGACAATTCCATTGGCAACCAGGATGGTTATGAATTTTGGAAA 60 	Qy 61 GATAGCGGTCGTGGGAATGATTCTCAATCATGGCGTACGTTCAGTGCCCAATGG 120	OY 121 AACAATGTTAACAACATATTACCGTAAAGGTAAAAATTCAATGAAACACAACAAC 180 	Oy 181 CAACAAGTTGGTAACATGTCCATAAACTACGGAGCCAACTTCCAACCAA	OY 241 TATTTATGCGTCTATGGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGT 300	Qy 301 TGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGA 360

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De,B.E., Lahaye,A., Ledoux,P. and Detroz,R.
Xylanase, microorganisms for its production, DNA molecules, process
of preparation and use thereof
Patent: EP 0698667-A 11 28-FEB-1996;
SOLVAX (BE)
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Other publication BE 100870 960604
Other publication BR 9503454 960305
Other publication PR 9503454 960305
Other publication FI 953578 960127
Other publication AU 2508695 960208
Location/Qualifiers
1. 1513
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Sequence 11 from Patent EP0698667.
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S. De, B. L. Lahaye, A. Ledoux, P. and Detroz, R. Xylanase, microorganisms for its production, DNA molecules, process of preparation and use thereof
L. Patent: EP 0698667-A 10 28-FEB-1996;
SOLVAY (BE)
Other publication BE 1008751 960702
Other publication BE 1008759 960604
Other publication BR 9503454 960409
Other publication FI 953578 960127
Other publication of PI 953578 960127
Other publication AD 2508659 960127
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/db_xref="taxon:32644"
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Patent: US 6346407-A 10 12-FBB-2002;
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100.0%; Score 663; DB 6;
Best Local Similarity 100.0%; Pred. No. 2e-169;
Matches 663; Conservative 0; Mismatches 0;
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SIKGIATFKQYWSVRRSKRTSGTISVSNHFRAWENLGMNMGKMYEVALTVEGYQSSGS
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/protein_id="CAB42305.1"
/db_xref="G1:4756811"
/translation="WRQKKLTFILAFLVCFALTLPABIIOAQIVTDNSIGNHDGYDYEFWRDSGGSTMILNHGGTFSAQWNNVNNILFRKGKKFNETQTHQQVGNMSINYGANFQPNGNAYLCYYGWTUADPLWSYYIVDSWGNWRPPGAPFKGTITVDGGTYDIYETLRNVNQPSNGATFKQYWSYRRSKRTSGTISVSNHFRAWENLGMNMGKMYEVALTVEGYQSSGSANVYSNTLRINGNPLSTISNDKSITLDKNN"
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                                                                                                                                                                             SP. AC13, NCIMB NO. 40482"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.7%; Score 634.2; DB 6;
llarity 97.3%; Pred. No. 1.4e-161;
Conservative 0; Mismatches 18;

    >744
/note="unnamed protein product"

1 (bases 1 to 744)
Dalboege, H., Diderichsen, B., Sandal, T. a
METHOD OF PROVIDING NOVEL DNA SEQUENCES
Patent: WO 9743409-A 1 20-NOV-1997;
NOVONORDISK AS (DK)
Location/Qualifiers
                                                                                                               1. .744
/organism="unidentified"
/mol_type="unassigned DNA"
/strain="BACILLUS SP. ACI3,
                                                                                                                                                                                                /db_xref="taxon:32644"
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les 645; Conserv
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AUTHORS
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De Buyl, E., Lahaye, A., Ledoux, P. and Detroz, R. Xylanase, microorganisms producing it, DNA molecules, methods preparing this xylanase and uses of the latter Patent: US 34846/7-A 11 12-FEB-2002; Location/Qualifiers
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Pred. No. 2e-169;
Mismatches 0; Indels
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from Patent WO9743409.
                                                                                                                            /organism="unknown"
/wol_type="unassigned
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                                                                                                        1. .1513
                                                                                                                                                                                                                                                        663; Conservative
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/codon_geratt=1
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                                                                                                                                       PAT 07-MAR-1997
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                                                                                                                                                                                                                                                                                                   1 (bases 1 to 744)
Van, S.P., Williams, D.P., Iverson, S., Farrell, R.L., Herbes, W.T.,
Van, D.K., Herweijer, M.A., Van, B.R., Quax, W.J., Goedegebuur, F. and
Jones, B.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTTTTGGAAA
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                                                                                                                                         linear
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96.4%; Pred. No. 5.8e-159;
iive 0; Mismatches 24;
                                                                                                                                         DNA
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Patent: WO 9518219-A 18 06-JUL-1995;
GIST BROCADES NV (NL)
Other publication UP 8507221T 960806
Other publication BR 9405934 951226
Other publication NO 953312 951019
Other publication NO 953312 951019
Other publication AU 1415095 950717.
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Sequence 18 from Patent WO9518219.
A45313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="unidentified"
/mol_type="unassigned DNJ/strain="1-43-3"
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Diderichsen, Balashedrge.
Method of providing a hybrid polypeptide exhibiting an activity
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0; Mismatches 18;
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Location/Qualifiers
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                                                                                                Sequence 1 from patent US 6270968.
AR163110
AR163110.1 GI:16233600
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Best Local Similarity 97.3%;
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Search completed: November 10, 2004, 21:26:27 Job time : 3210.21 secs

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Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suchizo-chou, Faurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattoriogsoc.riken.jp.) URL:http://hgp.gsc.riken.go.jp/,

Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9199

e-mail: abe@rtc.riken.jp
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Mus musculus molossinus DNA, clone:MSMg01-141H11.T7, genomic survey
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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BAC end Sequences of Library MSMg01
Unpublished
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90 est3: *
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90 est5: *
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E Jubases 1 to 865)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AG388392 865 bp DNA linear GSS 03-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-203120.TJ, genomic survey
                                                                                                                                                                                                            1225 AAAGAAGGTGAAGATCAAGAGAAATAACCATGCAAAAGTAAGAGAATAACTTTTAATAA 1166
                                                                                                                                                                                                                                                                 96 AACAGAGAAGGNCTGCATGAAAGGAGGTGATGGCTTTTTCATCTTAGGGATGACAGAACA 155
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                    36 AAAGGATTTATACACAAACAAGAGACATCCATGCCGGGTTAAAGCAGTATCGTTCCATCT
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
Unpublished
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                                            DB 9; Length 1281;
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/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .865
/organism="Mus musculus molossinus"
                                         Score 37.6; DB Fred. No. 2.1; Dr Mismatches
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/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-203120.TJ"
                                                                                                                                                                                                                                                                                                                                                                                           156 ATACGGATGAAAAAGGAGGGATGGAAA
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Mus musculus molossinus
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AG388392.1 GI:47999597
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                                                                                                          79; Conservative
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Sanger Institute
Hinkton, Cambridgeshire, CB10 1SA, UK
Email: tropeanger.ac.uk
Email: tropeanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TEGG105m20.plkSP6
Sequencing primer: SP6
Sequencing primer: SP6
Sequence is from a Xenopus Gene Collection (XGC) library
This sequence is from a Xorn.
CONSTRUCTED by Aaron M. Zorn.
CONSTRUCTED by 
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1 (bases 1 to 628)
Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
On Sep 15, 2002 this sequence version replaced gi:22888182.
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/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cE
was oligo dT primed from Sug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"
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Pred. No. 2.4;
); Mismatches 44; Indels (
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                                                                                                                                                                                                                                                                                                                                         141 AGGGATGACAGAACAATACGGATGAAAAAAGGAGGAGGGATGGAAA 185
                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="egg"
/lab_host="Escherichia coli XL1-blue"
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/mol type="mRNA"
/db_xref="taxon:8364"
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Xenopus tropicalis
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58.9%;
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Best Local Similarity 58.9
Matches 63; Conservative
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21 TATITCATITGTATCAAAGGATTTATACACAAACAAGAGACATCCATGCCGGGTTAAAGC

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880 bp mRNA linear EST 26-JUL-2004 CR584662 XGC-tailbud-head Xenopus tropicalis cDNA clone THdA042pl2 5', mRNA sequence.
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/lab_host="DH10B (phage-resistant)"
/clone lib="NIGHD XGC Emb8"
/note="Vector: pcWv-SPORT6.1; Site 1: Not1; Site_2: EcoRV; Cloned undirectionally. Primer: Oligo dT. Average insert size 2.1 kb. Constructed by Invitrogen. Note: This is a Xenopus Gene Collection (XGC) library."
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1 (bases 1 to 880)

1 (bases 1 to 880)

Sanger Xenopus tropicalis EST project 2001 (2004)

Unpublished (2004)
NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml.
Mational Institute of Child Health and Human Development, National
Cancer Institute, Xenopus Gene Collection
Unpublished (2002)
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Hinxton, Cambridgeshire, CB10 1SA, UK
Email: tropésanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: THAA042p12.p1kSP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Nigel Garrett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 20.1%; Score 37.2; DB 5; Length 663; 1 Similarity 58.9%; Pred. No. 2.5; 63; Conservative 0; Mismatches 44; Indels (
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| Corganism="Xenopus tropicalis"
| Mol type="mRNA" | Ab zref="taxon:8364"
| Clone="IMAGE:5381962"
| Lissue type="tadpole"
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/organism="Xenopus tropicalis"
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CR584662
                                                                   JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                              Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: tropeanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TEGG049199.plkSP6w
Sequencing Finner: BF
This sequence is from a Xenopus Gene Collection (XGC) library
Constructed by Aaron M. Zorn.
CDNA was oligo dT primed from 5ug of poly A+ RNA from egg.
ECORI-NOIL cut cDNA was then ligated into pCS107 with ECORI at the
S, end and Not1 at the 3' end.
Vector: pCS107; site 1: ECORI; Site 2: NotI
HOST: Escherichia coli Xil-blue.
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NISC no23g06.yl NICHD_XGC_Emb8 Xenopus tropicalis cDNA clone
IMAGE:5381962 5', mRNA sequence.
                          AL846715 AGC-egg Xenopus tropicalis cDNA clone TEgg049i19 5', mRNA
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Xenopus tropicalis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
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/lab_host="Escherichia coli XL1-blue"
/clome_lib="XGC-egg"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"
                                                                                                                                                                                        Eukariota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae, Xenopodinae, Xenopus, Silurana.

1 (bases 1 to 659)

1 (bases 1 to 659)

2 (croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (11_2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 TGATCTATTTCATTTGTATCAAAGGATTTTATACACAAGAGAGACATCCATGCCGGGTT
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Contact: Taylor R
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                                                                                                                                                      Xenopus tropicalis (western clawed frog)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TEgg049i19"
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BQ527682.1 GI:21386551
                                                                                                AL846715.2 GI:38487703
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Best Local Simil
Matches 63; C
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KEYWORDS
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/mod_type="genomic DNA"
/worl type="genomic DNA"
/worl type="genomic DNA"
/worl type="genomic DNA"
/worl traken="fetavon:5759"
/do xref="taxon:5759"
/do xref="taxon:5759"
/clone lib="Entamoeba histolytica Sheared DNA"
/rote="Weetor: pHOS1; Site:1: Bat 1; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond, LiS.
(1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing; projects: In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                          909 bp DNA linear GSS 14-NOV-2000 ENTGSG5TF Entamoeba histolytica Sheared DNA Entamoeba histolytica AZ549992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
Seg primer: M13-Forward
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Eukaryota; Entamoebidae; Entamoeba.
1 (basses 1 to 909)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library
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                                                    884 GAAGGAGTATGGCCCTGTCTACACTTTGTGGTCTGCATCTGAGGAG 838
                                                                                                                                                                   76 AAAGCAGTATCGTTCCATCTAACAGAGGAGGNCTGCATGAAAGGAGG 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
Contact: Brendan J Loftus
Contact: Brendan J Loftus
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD
Tel: 301 838 0208
Fax: 301 838 3543
     0; Mismatches
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High quality sequence stop: 762.
Location/Qualifiers
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Matches 87; Conserv
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Xenopus tropicalis

Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

E (Craniag, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (11_2003)

L (Onbach: Croning MDR

Sanger Institute

Hinxton, Cambridgeshire, CB10 1SA, UK

Email: trop@sanger.ac.uk

Sanger Xenopus tropicalis EST project 2001

TROPICALIS SEQUENCE_ID: TE99049914.q1kT)

Sequencing primer: T7

Nania Contaction (ARC) library
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EcoRI at the
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/clone_lib="XGC-egg"
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EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"
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/dev stage="tailbud head (stage 28-30)"
/dev stage="tailbud head (stage 28-30)"
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CDNA was oligo dT primed from 5ug of poly A+ RNA from egg.

ECORIANOII cut CDNA was then ligated into pCS107 with ECORI at 5, end and Not1 at the 3' end.

Vector: pCS107; Site 1: ECORI; Site 2: NotI

Host: Escherichia coli XL1-blue.
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20.1%; Score 37.2; DE
Best Local Similarity 58.9%; Pred. No. 2.6;
Matches 63; Conservative 0; Mismatches
                    mol_type="mRNA"
db_xref="taxon:8364"
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BX772034.1 GI:39679239
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58.9%;
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Best Local Similarity
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VERSION KEYWORDS SOURCE ORGANISM

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TITLE JOURNAL COMMENT AUTHORS

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RESULT 7

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RESULT 9

ઠે a SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL MEDLINE PUBMED

COMMENT

FEATURES

ACCESSION VERSION KEYWORDS

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Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre'
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBeloBACII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CR449406 352 bp mRNA linear EST 19-JUN-2004
CR444406 XGC-tailbud Xenopus tropicalis cDNA clone TTbA045k22 5',
mRNA sequence.
CR449406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 CATCTAACAGAAGANCTGCATGAAAGGAGGTGATGGGTTTTTCATCTTAGGGATGACA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus tropicalis
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Craniata; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 352)
Croning, M.D. R., Ashurst, J.L., Taylor, R., Garrett, N. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Croning MDR
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TTDA045k22.plkSP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Nigel Garrett.
Seq primer: SP6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 GTATCAAAGGATTTATACACAAACAAGAGACATCCATGCCGGGTTAAAGCAGTATCGTTC
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.4%; Score 35.8; DB 9; Length 1101; 27.1%; Pred. No. 7.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                         1. 1101

/organism="Drosophila melanogaster"

/mol type="genomic DNA"

/db xref="taxon:7227"

/clone="BACN37D12"

/clone lib="brosBAC"

/plasmid="pBelosAC11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 GAACAATACGGATGAAAAAAGGAGGGGATGGAAA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kenopus tropicalis (western clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 42; Conserv
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KEYWORDS
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JOURNAL
COMMENT
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CR449406
                                                                                                                            TITLE
JOURNAL
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                                                                                                                                                                                                CE215054 17000372924228 Dog Library Canis familiaris genomic, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Kirkness EF
He Institute for Genomic Research
Department of Eukaryolic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Rockville, MD 488-0200
Fax: 301-818-0208
Email: ekirknes@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           399 GAACCATTTTGTTCCAAATGAACACAGAATAACATAAAATTATGCATGGGTAAGTGATCC 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryo tamanana Karazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis. I bases 1 to 714)

Kirkness, E.P., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNS017L2
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN37D12 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             459 rigatritritracacticitatraccaargirgicaacatritragaagarcticcatagcregat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Canis familiaris"
/mol type="genomic DNA"
/strāin="Standard Poodle"
/db xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BsrXI; Libraries were prepared from peripheral blood"
                                                            703 ATTACAATTATTGGATGAAGGAAGAAGATACAGATGGGAGAAGAAGAAGACAGTTGGA 755
                                      183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                      131 TTTTCATCTTAGGGATGACAGAACAATACGGATGAAAAAAGGAGGGATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9; Length 714;
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Drosophila melanogaster
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AL108176
AL108176.1 GI:5628480
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CE215054.1 GI:35370723
                                                                                                                                                                                                                                                                                                                                                        Canis familiaris (dog)
                                                                                                                                                                                                                                                                                                                                                                               Canis familiaris
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82; Conserv
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

LOCUS DEFINITION

CNS017L2/c

RESULT 10

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Matches

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CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by Pieter de Jong"
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                                                                                 Score 35.6; DE
Pred. No. 7.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:8364"
/clone="THdA042p05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .874
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                                                                                   19.2%;
larity 59.6%;
Conservative
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Best Local Similarity
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                                                                                                                            59;
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Best Local Si
Matches 62;
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AL901596/c
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TITLE
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CR579359
                                                                                                                            Matches
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S Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
Riggs, F., de Jong, P. and Fraser, C.M.
Riggs, F., de Jong, P. and Fraser, C.M.
Lupublished (1999)
Other GSSs: CH230-351P2.TJ
Conteact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

Clones are derived from the rat BAC library availability.

(http://www.chori.org/bacpac/rat230.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/or ering_information.htm). BAC end

page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html

Plate: 351 row: p column: 2

Seg primer: T7

Class: BAC ends.
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CH230-351P2.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
CH230-351P2, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                        59 TGTACTAGATAAAATATCCCACAGAATTTATAAAGAACAAAAAAGACTATTATGAGGAATT 118
                                                                                       /dev_stage="tailbud (stage 28-30)"
/lab/host="Escherichia coli DH10B."
/clome lib="XGG-tailbud"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from Sug of poly A+ RNA from tailbud.
EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end.
                                                                                                                                                                                                                                                                                                                                                  Chordata, Craniata, Vertebrata, Euteleostomi,
Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Female"
|call_type=Brain"
|clone lib="CHORI-230 Segment 2"
|note="Vector: pTARBAC1.3; Site_1: Mbo1; Site_2: Mbo1;
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                 19.2%; Score 35.6; DB 7; Length 352; llarity 57.9%; Pred. No. 6.7; Conservative 0; Mismatches 45; Indels Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               76 AAAGCAGTATCGTTCCATCTAACAGAAGGNCTGCATGAAAGGAGG 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Rattus norvegicus"
            organism≕"Xenopus tropicalis"
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/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-351P2"
                                                 db xref="taxon:8364"
clone="TTbA045k22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                 type="mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BZ224970.1 GI:23883328
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                          Similarity
62; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BZ224970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus.
                                                                                                                                                                                                                                                                          Query Match
Best Local S
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KEYWORDS
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BZ224970/c
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874 bp mRNA linear EST 21-JUL-2004 CR579359 XGC-tailbud-head Xenopus tropicalis cDNA clone THdA042p05 CR579359 CR579359 641 retacriacaraaararcccaaacaarrraraaagaacacaaagacrarrarcagaarr 700 84 ATCGTTCCATCTAACAGAGGAGGACTGCATGAAAGGAGGTGATGGGTTTTTCATCTTAGG 143 /dev stage="Lailbud head (stage 28-30)"
/lab_host="Escherichia coli DH10B."
/clone_lib="XGG-tailbud-head"
/note="Vector: pCS107; Site_1: EcoR1; Site_2: Not1; CDNA was oligo dT primed from 5ug of poly A+ RNA from tailbud head. EcoR1-horI cut cDNA was then ligated into pCS107 with EcoR1 at the 5' end and Not1 at the 3' end." Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Sukaryotas (Bordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopodinae; Silurana. 1 (bases 1 to 874) Croning, M.D.R., Ashurst, J.L., Taylor, R., Garrett, N. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (2004) Unpublished (2004) Contact: Croning MDR
Sangar Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sangar.ac.uk
Sangar Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE ID: THGA042p05.plkSP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Nigel Garrett. 249 ATTTTCCTGTCTAACAATGGAGCAATGCATTTTCGGGTGTCTTGGGGTGGCCATTGCTGT Gaps Gaps ; 0 ó 76 AAAGCAGTATCGTTCCATCTAACAGAAGGNCTGCATGAAAGGAGG 122 701 gaagaagrargeccrercracacrrrcrecrecarcreadeaag 747 DB 7; Length 874; Length 833; 45; Indels Indels 144 GATGACAGAACAATACGGATGAAAAAGGAGGGATGG 182

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Unpublished (1999)
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Job time : 805.957 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hinakon, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE ID: TEGG021j23.q1kT7
Sequencing primer: T7
This sequence is from a Xenopus Gene Collection (XGC) library
Constructed by Aaron M. Zorn.
CDNA was oligo dT primed from Sug of poly A+ RNA from egg.
ECORI-NotI cut cDNA was then ligated into pCS107 with ECORI at the
5' end and NotI at the 3' end.
Vector: pCS107; Site 1: ECORI; Site_2: NotI
HOST: Escherichia coli XLL-blue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             951 bp mRNA linear EST 06-FEB-2001 mRNA sequence.
BG164591 GI:12671294
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       AL901596 AL-2003 960 bp mRNA linear EST 04-DEC-2003
AL901596 XGC-egg Xenopus tropicalis cDNA clone TEgg021j23 3', mRNA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 951)
                                                                                                                                                                                                                                                           Xenopus tropicalis
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                   L (bases 1 to 960)
Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
On Sep 16, 2002 this sequence version replaced gi:22953805.
Contact: Taylor R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rgraciagaraaariarcccaaagaarrraraaagaccaaaaagacrarrargaggaarr
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                          Kenopus tropicalis (western clawed frog)
                                                                                                                                                      AL901596.2 GI:38700171
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491 GGCCCACATAGAAGAAATGAATGAAAGACTTTAGAAAGCTTGGTGTGAAGCAAAACAG 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tiesue_type="hypernephroma, cell line"
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/clone lib="NIH MGC phage-resistant)"
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Site_2: Sal1; Cloned unidirectionally; oligo-dT_primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                    Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://mage.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 TATCAAAGGATTTATACACAAACAAGACATCCATGCCGGGTTAAAGCAGTATCGTTCC
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19.1%; Score 35.4; DB 4; Length 951;
Best Local Similarity 53.7%; Pred. No. 9.2;
Matches 72; Conservative 0; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  1. .951
/organism="Homo sapiens"
/mol_type="mRNR"
/db xref="taxon:966"
/clone="IMAGE:445255"
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 717. Location/Qualifiers
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Title: Perfect score:

Sequence:

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Run on: õ

Scoring table:

Searched:

Minimum DB E Maximum DB E

Database

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AR127019 Sequence
AR227049 Sequence
AR22003 Sequence
AR221306 Sequence
AR221305 Sequence
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AR22052B Bacillus
AF95091 Bacillus
AF95091 Bacillus
AF95091 Bacillus
AF36785 Bacillus
AC106432 Mus muscu
AC137318 Rattus no
AC137014 Rattus no
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AF528741 Sceloporu
AC09851 Homo Sapi
AC093430 Homo Sapi
AP004656 Oryza Sapi
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1 (bases 1 to 81)

1 betroz,R., Andre,C. and betroz,R., Andre,C. and betroz,R., Andre,C. and betrox,R.

Yetter,R.

Xylanase derived from a bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use
         A42251 Sequence 1
A42285 Sequence 35
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SOLVAY (BE)
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/db_xref="taxon:32644"
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Sequence 27 from Patent EP0634490.
A42277
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CR380952
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AC1337318
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AL160054
AF528741
AC098651
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A48248 Sequence 27
A4827042 Sequence 28
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AR220051 Sequence
AR220132 Sequence
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AR220134 Sequence
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            GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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unclassified
1 (bases 1 to 81)
De, B.E., Lahaye, A., Ledoux, P. and Detroz, R.
Xylanase, microorganisms for its production, DNA molecules, process
of preparation and use thereof
Patent: EP 0698667-A 28 28-FEB-1996;
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Pred. No. 2.4e-15;
; Mismatches 0; Indels
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Pred. No. 2.4e-15;
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Other publication BE 1008751 960702
Other publication BE 1008570 960604
Other publication BR 9503454 960305
Other publication JP 8092284 960409
Other publication AF 875578 960127
Other publication AV 2508695 960208.
Location/Qualifiers
Other publication AU 2508695 960208.
Location/Qualifiers
                                                                                                                                                             0; Mismatches
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/db_xref="taxon:32644"

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    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

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Sequence 28 from Patent EP0698667.
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tive 0;
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Best Local Similarity 100.0
Matches 81; Conservative
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(bases I (bases I) Ledoux, P. and Detroz, R.
Xylanase, microorganisms for its production, DNA molecules, process
of preparation and use thereof
Petent: BP 0698667-A 27 28-FEB-1996;
SOLVAY (BE)
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                                                                                                                                                                                                                                                 De, B.E., Lahaya, A., Ledoux, P., Amory, A., Detroz, R., Andre, C. and Vetter, R.
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Bacillus pumilus
Bacteria, Firmitutes; Bacillales; Bacillaceae; Bacillus.
1 (bases 1 to 81)
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Other publication BR 9402834 950613
Other publication F 7067637 950314
Other publication CA 2128050 950116
Other publication CA 2128050 950116
Other publication AU 6743294 950127
Other publication GB 2279955 950118.
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SOLVAY (BE)
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Sequence 27 from Patent EP0698667.
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Sequence 33 from Patent EP0634490.
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     61 ACGCCTGTGCCGGCTCATGCG 81
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A48248.1 GI:2302096
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1 (bases 1 to 81)
De Buyl, E., Lahaye, A., Ledoux, P. and Detroz, R.
Xylanase, microorganisms producing it, DNA molecules, methods for preparing this xylanase and uses of the latter
Patent: US 6346407-A 28 12-FEB-2002;
Location/Qualifiers
                                                                         Unclasses 1 to 81)

1 (bases 1 to 81)

De Buyl, E., Lahaye, A., Ledoux, P. and Detroz, R.

De Buyl, E., Lahaye, A., Ledoux, P. and Detroz, R.

Dreparing this xylanase and uses of the latter

Patent: US 6346407-A 27 12-FEB-2002;

Patent: US 6346407-A 27 12-FEB-2002;
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Sequence 27 from patent US 6423523.
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Sequence 28 from patent US 6346407.
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AR193073.1 GI:20239038
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1 (bases 1 to 81)
De Buyl, B., Lahaye, A., Ledoux, P., Amory, A., Detroz, R., Andre, C. and Vetter, R.
Xylanase derived from a bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use thereof
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De Buyl,E., Lahaye,A., Ledoux,P., Amory,A., Detroz,R., Andre,C. and
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Best Local Similarity 100.0%; Pred. No. 2.4e-15;
Matches 81; Conservative 0; Mismatches 0;
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100.0%; Score 81; DB 6; I
Best Local Similarity 100.0%; Pred. No. 2.4e-15;
Matches 81; Conservative 0; Mismatches 0;
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Location/Qualifiers
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Sequence 27 from patent US 6346407.
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/mol_type="unassigned DNA"

    .81
    /organism="unknown"
    /mol_type="unassigned DNA"

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Sequence 33 from patent US 6180382.
AR127047.
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     Sequence 27 from patent US 6180382.
AR127042
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1 (bases 1 to 81)
de Buyl,E., Lahaye,A., Ledoux,P., Amory,A., Detroz,R., Andre,C. and Vetter,R.
Xylanase derived from a Bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use thereof
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1 Similarity 100.0%; Pred. No. 2.4e-15;
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Sequence 30 from Patent EP0634490.
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Xylanase derived from a bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use thereof
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Sequence 27 from patent US 6426211.
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De,B.E., Lahaya,A., Ledoux,P., Amory,A., Detroz,R., Andre,C. and Vetter,R.
Xylanase derived from a bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
1 (bases 1 to 681)
De,B.E., Lahaya,A., Ledoux,P., Amory,A., Detroz,R., Andre,C. and
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100.0%; Score 81; DB 6; Length 681;
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Matches 81; Conservative 0; Mismatches 0; Indels
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Other publication BR 9402834 950613
Other publication CA 2128050 950116
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Other publication AD 674252 950116
Other publication AD 6742294 950127
Other publication GB 2279955 950118
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Deferon: EP 0634490-A 30 18-JAN-1995;
SOLVAY (BE)
Other publication NZ 260989 950828
Other publication BR 9402834 950613
Other publication FP 7067637 950314
Other publication CA 2128050 950116
Other publication NO 942652 950116
Other publication NO 942652 950116
Other publication AG 743294 950127
Other publication GB 2279955 950118.
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SOLVAY (BE)
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Sequence 32 from Patent EP0634490.
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Location/Qualifiers
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Sequence 30 from patent US 6180382.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Abli7799 Drosophil
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Anne60473 Sequence Add45341 Rat gene Ade56427 Rat gene Acf68431 Photorhab Acf65378 Photorhab Aag80923 B. pumilu Adj34969 DNA encod Aaq73997 Xylanase Description ABN66065 ABN71527_14 ABN71527_15 ADF77343_06 AAI93584 SUMMARIES ADD45341 ADE56427 ACF68431 ACF65378 ADP98598 AAN60473 AAQ80923 ADJ34969 ABL17799 ADE81488 AAC52006 AAC37584 ABV29555 ABV23689 ABL17798 AAQ73997 9 0 DB Query Match Length 1138 1216 1183 1183 1380 110000 110000 1905 2790 4106 1332 3623 100.0 100.0 98.0 37.0 28.6 28.4 28.4 28.4 Score 79.4 30 28.6 27.8 29.4 Š. Result υ υu υu

Continuation (12 o Ab127048 Drosophil Abn25404 Human ORF Aca35050 Prokaryot Asa81205 Drosophil Ass81203 DNA encod Aa81203 DNA encod Aak51700 Human pol Ab114055 Drosophil Ab114054 Drosophil Ad1059637 Rice heat Ad77245 Frog embr Ab172389 Castor lo Ab104066 Drosophil Ab113398 Drosophil Ab113398 Drosophil Ab113398 Drosophil Ab113398 Drosophil Ab13398 Human imm Ab1332668 Human imm Ab133268 Human imm Ab13268 Human imm	
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ALIGNMENTS

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AAQ73997 standard; DNA; 81

AAQ73997;

The Bacillus pumilus PRL B12 xylanase gene presequence (AAQ73997) encoding the xylanase signal peptide (AAR92055) was incorporated along with the promoter sequence (AAQ73996) into vectors used for the expression of DNA (see AAT1610) coding for a mature, thermostable xylanase (AAR92053) of Bacillus sp. 720/1. The enzyme is produced in transformed hosts, pref. Bacillus licheniformis or B. pumilus, for use in the paper pulp, animal feed and baking industries. (Updated on 16-OCT-Xylanase; thermostable enzyme; paper; pulp; bleaching; feedstuff; baking; Bacillus derived xylanase active over wide pH range - used in treatment of paper pulp, animal feeds and in bakery goods. Bacillus pumilus; strain PRL B12 (ATCC 55443) Detroz R; Ledoux P, Claim 27; Page 70; 94pp; English. promoter; signal peptide; ss. 95AU-00025086 94BE-00000706 95BE-00000448 (revised)
(first entry) Xylanase gene presequence. De Buyl E, Lahaye A, WPI; 1996-117341/13. P-PSDB; AAR92055. (SOLV) SOLVAY SA. 19-JUL-1995; 26-JUL-1994; 17-MAY-1995; 16-OCT-2003 15-MAY-1996 AU9525086-A 08-FEB-1996

Gaps

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Indels

Length 1022;

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The invention describes an isolated or recombinant polypeptide (1), having 50% or more identity to 190 300-1200 residue amino acid sequences (S1), given in the specification, over a region of 100 or more residues and the polypeptide as thermostable xylanase activity. (I) is useful for: dough conditioning, beverage production; as a mutritional supplement in animal feed; reducing lignin in a wood or a wood product; and for aliminating and protecting animals from a microorganism comprising xylan. The polymuclectide (II) encoding (I) is useful for amplifying nucleic acid encoding a polypeptide having a xylanase activity which involves amplifying (II) or its subsequence. (I) is useful for treating and preventing bacterial infection and fungal infection e.g. coccidiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibacterial; fungicide; thermostable xylanase activity; dough conditioning; beverage production; nutritional supplement; animal feed; lignin reduction; wood product; xylan; bacterial infection; fungal infection; coccidiosis; gene; ds.
recombinant plasmids carrying the xylanase gene. A chromosomal fragment obtained from isolate pBPX1 was subcloned and expressed in Escherichia coli JM109. The sequence of the xylanase gene (as a 1022 bp Sau3A1 fragment) carried by a selected transformant is given in AAQ80923
                                                                                                                                                                                                              1 ATGAATTTGAAAAGATTGAGGCTGTTGTTGTGATGTGTATTGGATTTGTGCTGACACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel xylanase recombinant polypeptide useful for improving textile texture, treating paper, eliminating microorganisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding xylanase from an environmental sample seq id 185.
                                                                                       Sequence 1022 BP; 329 A; 197 C; 229 G; 266 T; 0 U; 1 Other;
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100.0%; Pred. No. 5.1e-17;
ive 0; Mismatches 0;
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Esteghlalian A;
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P-PSDB; ADJ34970.
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/note= "base n at position 107 is not identified in the specification"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xylanase; endo-1,4-beta-D-xylanase; wood pulp; pulping; biobleaching; bleaching; bleaching; Bacillus licheniformis; ss.
                                                                                                               Gaps
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                                                                            Length 81;
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                                          BP; 16 A; 11 C; 26 G; 28 T; 0 U; 0 Other;
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                                                                         Query Match
100.0%; Score 81; DB 2; I
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 81; Conservative 0; Mismatches 0;
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/EC_number= "3.2.1.8"
/note= "claim 10"
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1. .185
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/note= "claim 12"
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/note= "claim 11"
267. .866
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186. .2
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P-PSDB; AAR68849.
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                                           Sequence 81
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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                    Drosophila melanogaster genomic polynucleotide SEQ ID NO 4867.
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11-JUL-2000; 2000US-00614150.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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pharmaceutical; gene; ds.
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                                    Length 684;
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Sequence 684 BP; 221 A; 129 C; 158 G; 176 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20; Indels
                                                                    Indels
                                Query Match 98.0%; Score 79.4; DB 12; Best Local Similarity 98.8%; Pred. No. 1.6e-16; Matches 80; Conservative 0; Mismatches 1;
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0; Mismatches
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                                                                                                                                                                           61 ACGCTGTGCCGCTCATGCG 81
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11-JUL-2000; 2000US-00614150
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7142 BP; 1604 A; 1620 C; 1812 G; 2106 T; 0 U; 0 Other;
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Pred. No. 9.1;
0; Mismatches 20; Indels
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Matches

Gaps

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16; Indels

0; Mismatches

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Sequence 508 BP; 165 A; 109 C; 90 G; 144 T; 0 U; 0 Other;
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                                                                                                           Rameaka JG,
Garcia CA,
                                19-JUN-2003
                                                                                                        Gorlach J,
                                                                                                                 Hurban P;
                gene; ss
                                                                    (PAGE/)
(MATH/)
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Best Local Similarity 70.9
Matches 39; Conservative
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25-MAR-1999;
29-MAR-1999;
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16-APR-1999;
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23-APR-1999;
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                                                                                genetically modified organism; transgenic organism; plant;
inhibitor testing; activator testing; modifier testing; fungicide;
insecticide; genetic function; genetic regulation; cellular metabolism;
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JP, Haas WD;
Hoffman N;
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                                 Arabidopsis thaliana expressed polynucleotide seq id 259
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A, Mathew AV, Ledford BL, Woessner
r M, Slater T, Davis KR, Allen K,
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Page A, Ma
Kricker M,
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LEDFORD B L.
WOESSNER J P.
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GARCIA C A.
KRICKER M.
SLATER T.
DAVIS K R.
ALLEN K.
HOFFMAN N.
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RAINES T M.
YU Y.
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Hybridisation assay, genetic mapping, gene expression control; protein identification; signal transduction pathway; metabolic pathway;
                                            159 Argcarcraraadcricardardardcriritririrgrirgdririgdartrigts 105
1 ATGAATTTGAAAAGATTGAGGCTGTTGTTTTGTGATGTGTATTGGATTTGTGCTGA 55
                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana DNA fragment SEQ ID NO: 70190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter; termination sequence; ss.
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9905-0132487P-
9905-01342863P-
9905-0134218P-
9905-0134219P-
9905-013421P-
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99US-0126264P.
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990S-0128234P.
990S-0128714P.
990S-0129845P.
990S-0130077P.
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99US-0130891P.
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99US-0132048P.
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99US-0137724P.
99US-0138094P.
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99US-0139119P.
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                                                                                                                                                                                        AAC52006 standard; DNA; 1138
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14-JUN-1999;

Length 508;

36.3%; Score 29.4; DB 10;

Query Match

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9908-0139452P.
9908-0139453P.
9908-0139454P.
9908-0139455P.
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9908-0139463P.
9908-0139453P.
9908-0140334P.
9908-0142054P.
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9908-014333P.
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9908-0144338P.
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9908-0144338P.
9908-014538P.
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Length 1138; DB 3; Score 29.4; DB Pred. No. 8.6; 0; Mismatches 9905-0150864P 9905-0150884P 9905-0151080P 9905-0151030P 9905-0151303P 9905-0151310P 9905-0151310P 9905-0152363P 9905-0153758P 9905-0153758P 9905-0153758P 9905-015473P 9905-015473P 9905-015563P 9905-015563P 9905-015563P 9905-015563P 9905-015563P 9905-015963P 99US-0160814P. 99US-0160818P. 99US-0160980P. 99US-016098P. 99US-0161404P. 99US-0161406P. 99US-0161359P. 99US-0161360P. 99US-0161920P. 99US-0161992P. 99US-0161993P. 99US-0162142P. 99US-0148565P. 99US-0148684P. 99US-0149175P. 99US-0149175P. 99US-0149722P. 99US-0149723P. 99US-0149723P. 36.3%; larity 70.9%; Conservative y Match . Local Similarity . Local 39; Conserv 13-AUG-1999; 13-AUG-1999; 10-AUG-1999; 10-AUG-1999; 20-AUG-1999; 20 04-0CT-1999 05-0CT-1999 06-0CT-1999 13-0CT-1999 13-0CT-1999 13-0CT-1999 14-0CT-1999 14-0CT-1999 14-0CT-1999 14-0CT-1999 14-0CT-1999 16-0CT-1999 17-0CT-1999 18-0CT-1999 Query Mai Besť Loca Matches

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16; Indels

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1 ATGAATTTGAAAGATTGAGGCTGTTGTTGTGATGTGTATTGGATTTGTGCTGA 55

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9905-0139459P.
9905-0139460P.
9905-0139460P.
9905-0139460P.
9905-0139461P.
9905-0139461P.
9905-0139621P.
9905-0140353P.
9905-0140354P.
9905-0140354P.
9905-0140354P.
9905-0140354P.
9905-014131P.
9905-014131P.
9905-014230P.
9905-014333P.
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29-JUN-1999;
30-JUN-1999;
01-JUL-1999;
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20-AUG-1999
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                 Arabidopsis thaliana DNA fragment SEQ ID NO: 17922.
                      AAC37584 standard; DNA; 1216 BP
                                                                                                                                                                    9905-0121825P.
9905-012180P.
9905-0125548P.
9905-01257848P.
9905-01257848P.
9905-01267482P.
9905-0128734P.
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9905-0138734P.
9905-0131449P.
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                                                   17-OCT-2000 (first entry)
                                                                                                             Arabidopsis thaliana
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18-JUN-1999;
18-JUN-1999;
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03-JUN-1999;
04-JUN-1999;
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10-JUN-1999;
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14-JUN-1999;
16-JUN-1999;
16-JUN-1999;
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28-MAY-1999;
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                                     AAC37584;
       RESULT 8
AAC37584
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cancer in a patient; (f) assessing the prostate cancer has metastasized in a patient; (h) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indohence of prostate cancer in a patient; (i) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                     Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 TGTTGTTTTGTGATGTGTATTGGATTTTGTGCTGACACTGACGGCTGTGCCGGCTCATGCG
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                            Human prostate expression marker cDNA 29546.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 6332-6333; 11750pp; English.
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25-MAY-2000) 2000US-0207454P.
09-UTIN-2000) 2000US-021314P.
13-UTI-2000) 2000US-0219007P.
13-DEC-2000) 2000US-0255281P.
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16-SEP-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-662795/76.
                                                                                                                                          WO200160860-A2
                                                                                                            Homo sapiens
                                                                                                                                                                        23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABV23689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABV23689/
ID ABV2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGAATTTGAAAAGATTGAGGCTGTTGTTTGTGATGTGTATTGGATTTGTGCTGA 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.3%; Score 29.4; DB 3; Length 1216;
ilarity 70.9%; Pred. No. 8.8;
Conservative 0; Mismatches והיחים
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1555/c
ABV29555 standard; cDNA; 1183 BP.
              9905-0149929P
9905-0149902P
9905-015066P
9905-015066F
9905-0151066P
9905-0151080P
9905-0151303P
9905-0151318
9905-0152363P
9905-0152363P
9905-0152363P
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990S - 01547799
990S - 01551399
990S - 0155659P
990S - 015658P
990S - 015658P
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9903-0157865P.
9903-0158202P.
9903-0158269P.
9903-0159293P.
9903-0159293P.
9903-0159231P.
9903-0159331P.
9903-0159331P.
9903-0159331P.
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99US-0160989P.
99US-0161404P.
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990S-0161920P.
990S-0161992P.
990S-0161993P.
990S-0162142P.
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99US-0160814P.
99US-0160815P.
99US-0160980P.
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99US-0161359P.
99US-0161360P.
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Best Local Similarity
Matches 39; Conserv
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13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
12-0CT-1999;
13-0CT-1999;
                                                             25-AUG-1999;
26-AUG-1999;
27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
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21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
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08-OCT-1999
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31-AUG-1999
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22-OCT-1

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ABV29555

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ABV29555, RESULT 9

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                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether progression of prostate cancer in b monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cancer in a patient; (f) assessing the prostate cancer in a patient; (f) determining whether prostate cancer has metastasized in a patient; (h)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antinflammatory; infection; vaccine; meningitis; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 TGTTGTGTGTGTGTGTATTGGGTTTTGTGCTGACACTGACGGCTGTGCCGGCTCATGCG 81
                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.3%; Score 28.6; DB 5; Length 1183; 67.8%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1183 BP; 311 A; 334 C; 321 G; 213 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus polynucleotide SEQ ID NO 43.
                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 4343-4344; 11750pp; English.
                                                                                                                                                                                                                                                    Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABN66065 standard; DNA; 1380 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
                                                                                                                 2000US-0189862P.
2000US-0207454P.
2000US-0211314P.
                                                                                                                                                                  18-JUL-2000; 2000US-0219007P.
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                                                                    20-FEB-2001; 2001WO-US005171
                                                                                                   2000US-0183319P
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                                                                                                                                                                                                                                                    Schlegel R, Endege WO,
                                                                                                                                                                                                                                                                                   WPI; 2001-662795/76.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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   WO200160860-A2
                                                                                                                   16-MAR-2000;
25-MAY-2000;
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                                                                                                   17-FEB-2000;
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                                    23-AUG-2001
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ABN66065
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The invention relates to a protein (ABP25413-ABP30895) from group B creptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the proteins have antibacterial and antiinflammatory activity. (1), nucleic acids encoding (1), ABN6604-ABN71526 and antibodies that bind (1) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (1) are used to detect Streptococcus in a compound binds to biological sample. (1) is used to detect Streptococcus in a compound binds to (1). A composition comprising (1) or a nucleic acid encoding (1), may be used to recombinantly produce (1) and may be caid encoding (1) may be used to recombinantly produce (1) and may be used in gene therapy. Antibodies to (1) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                          New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          732
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                                                                                                                                                                          Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGAATTTGAAAAGATTGAGGCTGTTGTTGTGATGTGTATTGGATTTGTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 28.4; DB 6; Length 1
Pred. No. 20;
0; Mismatches 16; Indels
                                                                                                                                                                          Masignani V, Margarit Y RosI, Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 3158; 4525pp; English.
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07-MAR-2001; 2001GB-00005640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus proteins
                                                                       (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC
                                                                                                                                                                                                                                                                                           WPI; 2002-352536/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
es 38; Conserv
                                                                                                                                                                                                                                                                                                                                 P-PSDB; ABP25434
                                                                                                                                                                                                                           rettelin H;
                                                                                                                                                                                     relford J,
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ABN71527 14/c Continuation (15 of 22) of ABN71527 from base 1400001 (Streptococcus polynucleotide WP Sequence split into 22 fragments LOCUS ABN71527 Accession Abn71527 810000 910000 1010000 110000 610000 1610000 1810000 2110000 210000 1310000 1410000 410000 510000 1110000 1210000 1510000 2010000 End 1900001 2000001 2100001 1100001 1200001 1300001 400001 500001 600001 700001 800001 900001 200001 1000001 1400001 Begin 100001 500003 1600003 170000 Fragment Name ABN71527 00 ABN71527 00 ABN71527 01 ABN71527 02 ABN71527 03 ABN71527 04 ABN71527_06 ABN71527_07 ABN71527_08 ABN71527_09 ABN71527_20 ABN71527_21 ABN71527_05 ABN71527_16 ABN71527_17 ABN71527 ABN71527 ABN71 ABN71 ABN71 ABN71 ABN71 RESULT 12

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73868 GTABABATTGATTTACCAGGATATTATCAATATTGGAATTATGCTGBABAGGTTAT 73927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymocleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, insue of conser, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65
                                                                                                                                                                                                                                                                                                                    Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                       68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITGAAAAGAITGAGGCTGITGTTTGTGATGTGTATTGGATTTGTGCTGACACTGACGGC
                                                       9 GAAAAGATTGAGGCTGTTTGTGATGTGTATTGGATTTGTGCTGACACTGACGCCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3623 BP; 1143 A; 501 C; 572 G; 1303 T; 0 U; 104 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the printed specification, but was obtained in electronic for directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Score 28; DB 10; Length 110000; Pred. No. 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 27.8; DB 4; Length 3623; Pred. No. 41; 0; Mismatches 22; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 13644; 1399pp + Sequence Listing; English.
                              0; Mismatches
                                                                                                                                                                                                                                                                                            Human polynucleotide SEQ ID NO 13644.
                                                                                                                                                                                                            AAI93584 standard; cDNA; 3623 BP
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llarity 65.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-2001; 2001WO-US004927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2000; 2000US-00515126
18-MAY-2000; 2000US-00577409
 Query Match
Best Local Similarity 63.2%;
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fang YT, Liu C, Drmanac
                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                  73928 GCCGGCAC 73935
                                                                                                               69 GCCGGCTC 76
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AA013653
                                                                                                                                                                                                                                                                                                                                                                                                                        WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                  trinuation (16 of 22) of ABN71527 from base 1500001 (Streptococcus polynucleotide SEQ Sequence split into 22 fragments LOCUS ABN71527 Accession Abn71527
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                                                                                        Gaps
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                                              Gaps
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                 Length 110000,
                                                                          ATGAATTTGAAAAGATTGAGGCTGTTGTTTGTGATGTGTATTGGATTTG
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                                              Indels
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                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6;
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                     B
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                  Score 28.4; DB
Pred. No. 67;
0; Mismatches
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2110000
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1110000
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2100001
                    Query Match
Best Local Similarity 70.4%;
Matches 38; Conservative
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Continuation (16 of 22)
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Best Local Similarity
Matches 38; Conserv
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Continuation (7 of 20)
WP Sequence split into
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ADF77343 00
ADF77343 01
ADF77343 02
ADF77343 03
ADF77343 04
ADF77343 06
ADF77343 06
ADF77343 06
ADF77343 06
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ABN71527 00
ABN71527 00
ABN71527 02
ABN71527 04
ABN71527 04
ABN71527 06
ABN71527 06
ABN71527 06
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ABN71527-15
ABN71527-16
ABN71527-16
ABN71527-18
ABN71527-19
ABN71527-21
ABN71527-21
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ADF77343_19
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ADF77343_13
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ADF77343_1
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ABN71527_1
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ADF77343 0
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2724 TIGAATAAGATATATGATATTGATTCTGAGCTGCTTTGTATTTTTTCTGACTTTGGCATC 2783 g

66 TGT 68 |||| 2784 TGT 2786

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Search completed: November 10, 2004, 17:09:40 Job time : 54.3814 secs

1859 v

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; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
US-08-275-526C-27
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STRANDEDNESS: single
                                                                           21, Appl
1889, Ap
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                                                                                                                                                                                                                                                                                                            1 ATGAATTTGAAAAGATTGAG.......CGGCTGTGCCGGCTCATGCG 81
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.: /cgn2 = /ptodata/1/ina/6A_COMB.seq:*
.: /cgn2 = /ptodata/1/ina/6E_COMB.seq:*
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.: /cgn2 = /ptodata/1/ina/PcTUS_COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-073-055-1
US-09-073-055-35
US-09-270-767-213499
US-09-248-796A-2584
US-09-248-796A-2584
US-09-248-796A-2584
US-09-248-796A-223
US-10-204-708-21
US-09-313-294A-1889
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US-08-470-953A-27
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US-09-076-677-33
US-09-076-677-33
US-09-073-055-37
US-09-073-055-37
US-09-075-526C-30
US-09-073-055-32
US-09-073-055-32
US-09-073-055-32
US-09-073-055-32
US-09-073-055-32
US-09-073-055-32
US-08-275-526C-3
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Maximum Match 100%
Listing first 45 summaries
                                                                                                    sw model
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Gapop 10.0 , Gapext 1.0
                                                                                                         nucleic search, using
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Maximum DB seq length: 2000000000
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81
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27.8
26.2
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Perfect score:
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              Length 81;
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                                                                                    1 ATGAATTTGAAAAGATTGAGGCTGTTGTTTTGTGATGTGTATTGGATTT
                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C. STREET: 2000 K.St., N.W., Suite 200 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/275,526C
FILING DATE: 15-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e-19;
Matches 81; Conservative 0; Mismatches 0;
            Score 81; DB 3; I
Pred. No. 1.8e-19;
Sequence 33, Application US/08275526C Patent No. 6180382 GENERAL INFORMATION APPLICANT: DE BUYL, ERIC APPLICANT: LAHAYE, ANDR E
                                                                                                                                                        61 ACGCTGTGCCGGCTCATGCG 81
                                                                                                                                                                                         61 Accertarccccccrcarccc 81
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ATTORNEY/AGENT INFORMATION:
NAME: Gadiano, Wilhlem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-0625
TELEFAX: 620 383 5605
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: genomic DNA ORIGINAL SOURCE: ORGANISM: Bacillus pumilus STRAIN: PRL B12
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                                                                                                                                                                                                                                                                                                                                                 LAHAYE, ANDR E
LEDOUX, PIERRE
AMORY, ANTOINE
                Query Match
Best Local Similarity 100.
Matches 81; Conservative
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT:
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APPLICANT: ANDREE LAHAYE
APPLICANT: PIERRE LEDUX
APPLICANT: PIERRE LEDOUX
APPLICANT: PIERRE LEDOUX
APPLICANT: PIERRE LEDOUX
TITLE OF INVENTION: Xylanase, microorganisms produced it,
TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 2000 K St., N.W., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,953A
FILING DATE: 6-OCTOBER-1995
CLASSIFICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 81; DB 3; I 100.0%; Pred. No. 1.8e-19; tive 0; Mismatches 0;
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US-08-470-953A-28
Sequence 28, Application US/08470953A
Patent No. 6346407...
                                                                                                                                               ; Sequence 27, Application US/08470953A; Patent No. 6346407; GENERAL INFORMATION:
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81
                                        61 ACGGCTGTGCCGGCTCATGCG 81
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ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, ESG
REGISTRATION NUMBER: 37,136
FREFRENCE/DOCKET NUMBER: 4121
FLERCOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625
TELEPHONE: 202-429-0625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 Accerrarcccccrcarcc
61 ACGGCTGTGCCGGCTCATGCG
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INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic) US-08-470-953A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 100.
Matches 81; Conservative
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LENGTH: 81 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: D.C
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EXPRESSION VECTORS FOR SUCH XYLANASE AND
OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
USE THEREOF
EXPRESSION VECTORS FOR SUCH XYLANASE AND OTHER PROTEINS, HOST ORGANISMS THEREFOR AND USE THEREOF
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CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 81; DB 4; Length 81; 100.0%; Pred. No. 1.8e-19; ive 0; Mismatches 0; Indels
                                                                                                  ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, STREET: 2000 K St., N.W., Suite 200
                                                                                                                                                                                                    ZIP: 2006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,677
                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 12-May-1998
CLASSIFICATION: «Unknown»
PRIOR APPLICATION LATA:
APPLICATION NUMBER: US 08/275,526
FILING DATE: 15-UL-1994
ATTORNEY, AGENT INFORMATION:
NAME: Gadiano, Wilhiem F.
REGISTRATION NUMBER: 37,136
REFERENCE, POCKET NUMBER: 4121-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEPRAX: (202) 293-0625
TELEPRX: 650 383 5605
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: genomic DNA SEQUENCE DESCRIPTION: SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33, Application US/09076677
Patent No. 6423523
GENERAL INFORMATION:
APPLICANT: DE ALAHNER, ANDREE
LEDOUX, PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ACGGCTGTGCCGGCTCATGCG 81
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ANDRE, CHRISTOPHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                             NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN
                                                                                                                                             CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81; Conservative
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Best Local Similarity
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                                                                                     Xylanase, microorganisms produced it,
DNA molecule, processes for preparation of this xylanase
and uses thereof
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                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Ploppy disk

COMPUTER: PLOPEN FC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/470,953A

FILING DATE: 6-OCTOBER-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:
                                                                                                                                          ALIONE STREE: WILLIAN BRINKS HOFER GILSON & LIONE STREE: 2000 K St., N.W., Suite 200 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 81; DB 3; I
Pred. No. 1.8e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICALL...

PILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION UNUBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:
TELEFAK: (202, 293-1850
TELEFAK: (202) 293-1850
TELEK: 60 383-5605
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
""" (cenomic)
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Patent No. 6423523
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMORY, ANTOINE
DETROZ, RENE
ANDRE, CHRISTOPHE
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LAHAYE, ANDREE
LEDOUX, PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
                             ERIC DE BUYL
PIERRE LEDOUX
                                                                                       TITLE OF INVENTION: Xyl
TITLE OF INVENTION: DNA
TITLE OF INVENTION: and
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                        RENE DETROZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 1..81
                                                                                                                                                                                                                                                            STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-470-953A-28
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APPLICANT: DE BUYL, ERIC
LEBOUX, PIERRE
AMORY, ANOINE
DETROZ, REN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 81 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                   ZIP: 20006
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
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US-09-073-055-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES
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CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFFR GILSON & LIONE, P.C.
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 81;
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                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 81; DB 4; I
Best Local Similarity 100.0%; Pred. No. 1.8e-19;
Matches 81; Conservative 0; Mismatches 0;
STREET: 2000 K St., N.W., Suite 200
                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,677
FILING DATE: 12-May-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/275,526
                                                                                                                                                                                                                                                                                                                             ATTOREY/AGENT INFORMATION:
NAME: Gadiano, Wilhlem F.
REGISTRATION NUMBER: 37,136
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELEPHONE: (202) 429-0625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN: PRL B12
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-076-677-33
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Patent No. 6426211
GENERAL INFORMATION:
APPLICANT: DE BUYL, ERIC
LAHAYE, ANDR E
LEDOUX, PIERRE
LEDOUX, ANDR E
LEDOUX, ANDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMORY, ANTOINE
DETROZ, REN
ANDRE, CHRISTOPHE
VETTER, ROMAN
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TELEX: 650 383 5605
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 81 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: genomic DNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ropology: linear
                                  STATE: D.C.
COUNTRY: U.S.A.
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1 ATGAATTTGAAAAGATTGAGGCTGTTGTTTGTATTGTGTTTGTGCTGACACTG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VETTER, ROMAN TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGAATTTGAAAAGATTGAGGCTGTTGTTTTGTGATGTGTATTGGATT
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
CERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 81; DB 4; I
Best Local Similarity 100.0%; Pred. No. 1.8e-19;
Matches 81; Conservative 0; Mismatches 0;
                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/073,055
FILING DATE: 05-May-1998
CLASSIFICATION: AUKnown>
PRIOR APPLICATION: AUKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/275,526
FILING DATE: 15-UUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gadiano, Wilhlem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-49
TELEFPHONE: (202) 429-0625
TELEFPHONE: (202) 293-0625
TELEFPHONE: (202) 293-0625
TELEFPKX: (202) 293-0625
TELEFKX: (202) 293-0625
TELEFRY: (202) 293-0625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ACGGCTGTGCCGGCTCATGCG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ACGCTGTGCCGCTCATGCG 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANDRE, CHRISTOPHE
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1 ATGAATTTGAAAAGATTGAGGCTGTTGTTTTGTGTGTTTTGGATTTGTGCTGACACTG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 81; DB 3; Length 681; Best Local Similarity 100.0%; Pred. No. 3.8e-19; Matches 81; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C. STREET: 2000 K St., N.W., Suite 200
                                                                                                   4121-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 32, Application US/08275526C; Patent No. 6180382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AccertarcccccrtcArccc 81
                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gadiano, Wilhlem F.
REGISTRATION NUMBER: 37,136
REPERENCE/DOCKET NUMBER: 4121
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Gadiano, Wilhlem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 412
TELECOMMUNICATION INFORMATION:
TELERAN: (202) 429-0625
TELERA: 650 383 5605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ACGGCTGTGCCGGCTCATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DE BUYL, ERIC
LAHAYE, ANDR E
LEDCOUX, PIERRE
AMORY, ANTOINE
DETROZ, REN
ANDRE, CHRISTOPHE
VETTER, ROMAN
                                                                                                                                    TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-0625
TELEFAX: 650 383 5605
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 681 base pairs
TYPE: nucleic acid
STRANDEDNESS: 81ngle
                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
15-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DE BUYL, BE
APPLICANT: LAHAYE, ANI
APPLICANT: LEDOUX, PIE
APPLICANT: DETROCX, REN
APPLICANT: DETROCX, REN
APPLICANT: NETRE, ROWA
TITLE OF INVENTION: EXP
TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 35
CORRESPONDENCES: 35
ADDRESSER: MADDRESSES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-275-526C-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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    SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 2006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPPY Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 81; DB 4; L
100.0%; Pred. No. 1.8e-19;
rative 0; Mismatches 0;
        CURRENT APPLICATION DATA:

RAPLICATION NUMBER: US/09/073,055
FILING DATE: 05-May-1998
CLASSIFICATION NUMBER: US/09/073,055
FILING DATE: 05-May-1998
CLASSIFICATION NUMBER: US/08/275,526
FILING DATE: 15-UUL-1994
ATTORNEY/ACENT INFORMATION:
NAME: Gadiano, Wilhlem F.
REGISTATION NUMBER: 4121-49
TELEFAX: (202) 293-0625
TELEFAX: (202) 293-0625
TELEFAX: (50 383 5605
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: uncleic acid
STRANDEDNESS: single
TYPE: uncleic acid
STRANDEDNESS: single
TYPE: UNCLEIC acid
STRANDEDNESS: single
TYPE: TYPE: Genomic DNA
ONIGLIAL SOURCE:
ONIGLIAL SOURCE:
ONIGLIAL SOURCE:
ONIGLIAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Bacillus pumilus
STRAIN: PRL B12
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-073-055-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/275,526C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DE BUYL, ERIC
APPLICANT: LAHAYE, ANDR E
APPLICANT: LEDOUX, PIERRE
APPLICANT: AMORY, ANTOINE
APPLICANT: BETROZ, REN
APPLICANT: ANDRE, CHRISTOPHE
APPLICANT: VETTER, ROMAN
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: CHRISTROPHE
TITLE OF INVENTION: CHRISTROPHE
TITLE OF INVENTION: CHRISTROPHE
TITLE OF INVENTION: USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 81; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN E
STREET: 2000 K St.,
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TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
EXPRESSION VECTORS FOR SUCH XYLANASE AND
OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE, P.C. STREET: 2000 K St., N.W., Suite 200 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Tam PC compatible
CORRESTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,677
FILING DATE: 12-May-1998
CLASSIFICATION: <Unknown>
                                                                                                                                   Length 681,
                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                            1 ATGAATTTGAAAAGATTGAGGCTGTTGTTTGTGATGTGTA
                                                                                                                              100.0%; Score 81; DB 4; 1
100.0%; Pred. No. 3.8e-19;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/275,526
FILING DATE: 15-7UL-1994
ATTONNEY/AGENT INFORMATION:
NAME: Gadiano, Wilhlem F.
REGISTRATION NUMBER: 37,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 4121-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
                    TOPOLOGY: linear

MOLECULE TYPE: genomic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
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STRAIN: PRL B12
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DETROZ, RENE
ANDRE, CHRISTOPHE
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US-09-076-677-32
i Sequence 32, Application US/09076677
j Patent No. 6423523
j GENERAL INFORMATION:
j APPLICANT: DE BUYL, ERIC
j APPLICANT: DE MADREE
                                                                                                                                                                                                                                                                                                               81
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TELEX: 650 383 5605
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                  61 ACGCTGTGCCGGCTCATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: genomic DNA ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 81; Conservative
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LEDOUX, PIERRE
AMORY, ANTOINE
DETROZ, RENE
ANDRE, CHRISTOPHE
VETTER, ROWAN
TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
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                                                                                                                                                                                                                                                                    Length 681;
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 81, DB 3, I
Best Local Similarity 100.0%; Pred. No. 3.8e-19;
Matches 81; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/275,526
FILING DATE: 15-UUL-1994
ATTORREY/AGENT INFORMATION:
NAME: Gadiano, Wilhlem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-0625
TELEFAX: 650 389 5605
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 12-May-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ACGCCTGTGCCGGCTCATGCG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 30, Application US/09076677
Patent No. 6423523
GENERAL INFORMATION:
APPLICANT: DE BUYL, ERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 681 base pairs
TYPE: nucleic acid
                                                                                                                                                                       ORGANISM: Bacillus pumilus
STRAIN: PRL B12
                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington STATE: D.C. COUNTRY: U.S.A.
                                         LENGTH: 681 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRE
                                                                                                                                                                                                                        US-08-275-526C-32
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1 ArcaArricaAaAcArricaGccrcrrcrrcrcaArgrcrarrcGArricaAcacrc 60
               ATGAATTTGAAAAGATTGAGGCTGTTGTTTGTGATGTATTGGATTTGTGCTGACACTG
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EXPRESSION VECTORS FOR SUCH XYLANASE AND
CYHER PROTEINS, HOST ORGANISMS THEREFOR AND
USE THEREOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K St., N.W., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 81; DB 4; Length 681; ilarity 100.0%; Pred. No. 3.8e-19; Conservative 0; Mismatchen n. Trani
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FILING DATE: 15-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gadiano, Wilhlem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1:0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/073,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Bacillus pumilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 05-May-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION TELEPHONE: (202) 429-062
                                                                                                                                                                                                                                               Sequence 32, Application US/09073055
Patent No. 6426211
GENERAL INFORMATION:
APPLICANT: DE BUYL, ERIC
                                                                                                 81
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MEDIUM TYPE: Floppy disk
                                                                                                                                         61 Acecrerecececrearece 81
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TELEX: 650 383 5605
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                     ANDRE, CHRISTOPHE
VETTER, ROMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 681 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
                                                                                                   61 ACGCCTGTGCCGCCTCATGCG
                                                                                                                                                                                                                                                                                                                                   LAHAYE, ANDR E
LEDOUX, PIERRE
                                                                                                                                                                                                                                                                                                                                                                             AMORY, ANTOINE
DETROZ, REN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 81; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
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                                                                                                                                                                                                         RESULT 14
US-09-073-055-32
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                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 81; DB 4; Length 681; Best Local Similarity 100.0%; Pred. No. 3.8e-19; Matches 81; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IS Floppy disk
COMPUTER: The PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,055
FILING DATE: 05-May-1998
CLASSIFICATION: <understandard.
                                                              Length 681;
                                                                                                     Indels
                                                              core 81; DB 4; I
red. No. 3.8e-19;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/275,526
FILING DATE: 15-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VETTER, ROMAN
TITLE OF INVENTION: XYLANASE DERIVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-073-055-30
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
                                                              Score 81;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Gadiano, Wilhlem F.
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 30, Application US/09073055
Patent No. 6426211
GENERAL INFORMATION:
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TELEX: 650 383 5605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 681 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                    1 ATGAATTTGAAAAGATTGAGGC
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                                                                                                                                                                                                                                    61 ACGCTGTGCCGGCTCATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DE BUYL, ERIC
LAHAYE, ANDR E
LEDOUX, PIERRE
                                                           uvery match 100.0%;
Best Local Similarity 100.0%;
Matches 81; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-09-073-055-30
      ;
US-09-076-677-32
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186 ATGAATTTGAAAAGATTGAGGCTGTTGTTGTTGTGTGTATTGGATTTGTGCTGACACTG 245
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1 ATGAATTTGAAAAGATTGAGGCTGTTGTTTGTGATGTGTATTGGATTTGTGCTGACACTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                              XYLANASE DERIVED FROM A BACILLUS SPECIES, EXPRESSION VECTORS FOR SUCH XYLANASE AND OTHER PROTEINS, HOST ORGANISMS THEREFOR AND USE THEREOF 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 81; DB 3; Length 1022; Best Local Similarity 100.0%; Pred. No. 4.3e-19; Matches 81; Conservative 0; Mismatches 0; Indels
                                                                                                           61 ACGGCTGTGCCGGCTCATGCG 81
                                                                                           Sequence 1, Application US/08275526C Patent No. 6180382
                    61 ACGGCTGTGCCGGCTCATGCG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
ORGANISM: Bacillus pumilus
STRAIN: PRL B12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-275-526C-1
                                                                        RESULT 15
US-08-275-526C-1
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Search completed: November 11, 2004, 01:34:29
Job time : 11.3051 secs
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November 10, 2004, 21:26:43; Search time 51.7881 Seconds (without alignments) 8421.106 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGAATTTGAAAAGATTGAG.........CGGCTGTGCCGGCTCATGCG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications NA:*

1: /cgn2 6/ptodata/1/pubpna/USO7 PUBCOMB.seq:*
2: /cgn2 6/ptodata/1/pubpna/DEG NEW PUB.seq:*
3: /cgn2 6/ptodata/1/pubpna/USO6 NEW PUB.seq:*
4: /cgn2 6/ptodata/1/pubpna/USO6 PUBCOMB.seq:*
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8: /cgn2 6/ptodata/1/pubpna/USO8 NEW PUB.seq:*
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11: /cgn2 6/ptodata/1/pubpna/USO9B PUBCOMB.seq:*
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14: /cgn2 6/ptodata/1/pubpna/USO0 NEW PUB.seq:*
15: /cgn2 6/ptodata/1/pubpna/USO0 PUBCOMB.seq:*
16: /cgn2 6/ptodata/1/pubpna/USO0 PUBCOMB.seq:*
17: /cgn2 6/ptodata/1/pubpna/USO0 NEW PUB.seq:*
18: /cgn2 6/ptodata/1/pubpna/USO0 NEW PUB.seq:*
19: /cgn2 6/ptodata/1/pubpna/USO0 NEW PUB.seq:*
20: /cgn2 6/ptodata/1/pubpna/USO0 NEW PUB.seq:*
21: /cgn2 6/ptodata/1/pubpna/USO0 NEW PUB.seq:*
22: /cgn2 6/ptodata/1/pubpna/USO0 NEW PUB.seq:*
22: /cgn2 6/ptodata/1/pubpna/USO0 NEW PUB.seq:*
22: /cgn2 6/ptodata/1/pubpna/USO0 NEW PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3611042 seqs, 2692057975 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                         sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                         nucleic search, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                       US-09-909-207-27
81
                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                            OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                                                                                               Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			de			SUMMARIES	
Result No.	ult No.	Score	Query Match	Query Match Length DB	08	ID	Description
	-	81	100.0	81	6		Sequence 27, Appl
	~	81	100.0	81	σ	US-09-909-207-28	Sequence 28, Appl
U	m	29.4	36.3	508	10	US-09-770-961-259	Sequence 259, App
	4	29	35.8	2363	13	US-10-027-632-263227	Sequence 263227,
	'n	5	35.8	2363	13	US-10-027-632-263228	Sequence 263228,
	9	5	35.8	2363	15	US-10-027-632-263227	Sequence 263227,
	7	5	35.8		15	US-10-027-632-263228	Seguence 263228,
	00	28.8	35.6	233060	13	US-10-087-192-97	Sequence 97, Appl
	σ	28	34.6		13	US-10-087-192-1615	Sequence 1615, Ap
U	10	28	34.6	87731	13	US-10-087-192-1342	Sequence 1342, Ap
υ	11	27.6	34.1	614	18	US-10-425-115-162687	Sequence 162687,
	12	27.6	34.1	1383	18	US-10-425-115-137066	Sequence 137066,

71 Sequence 83971, A	3 Sequence 1	4 Sequence	7 Sequence 60737,	Sequence	3 Sequence 41153,	1 Sequence		Seguence	920 Sequence	10938	•	Sequence 4	Sequence	Sequence	2 Sequence	3 Sequence 7624	Seguence	16337	8 Sequence 163378	Sequence 1622,	sedneuce	7	Sequence 59754		6 Sequence 1296		641,	Sequence	Sequence 352,	2 Sequence 535	4 Sequence 2014	
18 US-10-425-115-8397	10-437-963	10-4	10-425-115	US-10	-10-369-493-4	US-10-424-5	US-10	18 US-10-739-930-210	US-10-282-122A-2	16 US-10-424-599-109	63	9 US-09-910-943-478	16 US-10-425-114-3098	18 US-10-425-115-6665	16 US-10-425-114-35562	us-	US-10-410-031-16	US-10-027-632-16	US-10-027-632	16 US-10-424-599-1622	US-10-425-114	US-10-425-114-1	US-10-425-115-5	US-10-424-599-1	15 US-10-311-455-129	US-10-204	US-10	US-10-240-589C-	US-10-128-714-3	US-10-128-714-5		
263	648	1763	1128	193853	681	343	454	5755	363	2274	324	727	990	1052	1278	1681	1959	401	401	404	1011	1932	2160	2354	9741	11049	11049	11049	2896	2897	248436	
33.8		33.8	33.6	33.6	33.3	33.1	33.1	33.1	32.8	32.6	32.3	32.3	32.3	32.3	32.3	32.3	32.3	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1	31.9	31.9	31.9	
27 4	4.70	4 70		27.2	27	26.8	26. A	26.8	26.6	26.4	26.2	26.2	26.2	26.2	26.2	26:2	26.2	26		26	26	26	26	26	26	26	26	26	S	25.8	25.8)
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ALIGNMENTS

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RESULT 1

US-09-207-27

US-09-207-27

Sequence 27, Application US/09909207

Patent No. US20201518141

GENERAL INFORMATION:

GENERAL INFORMATION:

PIERRE LEBOUX

RENE DETRO

PIERRE LEBOUX

RENE DETRO

ITILE OF INVENTION: Xylanase, microorganisms produced it,

DIA molecule, processes for preparation of this xylanase and uses thereof

NUMBER OF SEQUENCES:

ADDRESSES:

ADDRESSES:

ADDRESSES:

CORRESPONDENCE ADDRESS:

ADDRESSES:

ADDRESSES:

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSES:

CORPTER: 1500 K St., N.W., Suite 200

STATE: D.C.

COMPUTER: 1504 C compatible

COMPUTER: 1504 C compatible

COMPUTER: 1504 C compatible

COMPUTER: PADABLE PORM:

MEDIUM TYPE: Floppy disk

COMPUTER: PADABLE PORM:

MEDIUM TYPE: PLOPPY disk

COMPUTER: PADABLE PORM:

MEDIUM TYPE: PLOPPY disk

COMPUTER: PADABLE PORM:

MEDIUM TYPE: PLONDY disk

COMPUTER: PADABLE PORM:

MEDIUM TYPE: PLONDY disk

COMPUTER: PADALICATION NUMBER: 08/09/909,207

FILING DATE: 19-Jul-2001

CLASSIFICATION NUMBER: 08/10,953

FILING DATE: 06-JUNE-1995

PURDERALING DATE: 06-JUNE-1995

ATTORNEY APPLICATION NUMBER: 08/10,953

FILING DATE: 06-JUNE-1995

REGISTRATION NUMBER: 37,136

NUMBER: 91,136
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1 ATGAATTTGAAAAGATTGAGGCTGTTGTTTGTGATGTGTATTGGATTTGTGCTGACACTG 60
                                                                                                                                                                                                                                           1 ATGAATTTGAAAAGATTGAGGCTGTTGTTTTGTGTGTTTTGGATTTGTGCTGACACTG
                                                                                                                                                                                                         Gaps
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                                                                                                                                                                 Length 81;
                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith R.
APPLICANT: Hoffman, Neil
APPLICANT: Hoffman, Neil
APPLICANT: HUSAN: Hushan, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REPERENCE: 2026 (FARA-0159RV)
CURRENT APPLICATION UNMER: US/09/770,961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
                                                                                                                                                             ; Score 81; DB 9; I
; Pred. No. 1.1e-17;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 29.4; DE
Pred. No. 6.5;
0; Mismatches
                                                                              LOCATION: 1..81
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 259
LENGTH: 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-027-632-263227
; Sequence 263227, Application US/10027632
; Publication No. US20020198371A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,466
PRIOR FILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-770-961-259/c
; Sequence 259, Application US/09770961
; Publication No. US20030115639A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     61 ACGCTGTGCCGGCTCATGCG 81
                                                                                                                                                                                                                                                                                                                              61 ACGGCTGTGCCGGCTCATGCG 81
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page, Amy
Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
Garcia, Carlos A.
                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Arabidopsis thaliana US-09-770-961-259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.3%;
70.9%;
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Rameaka, Joshua G.
                                                                                                                                                                                                       81; Conservative
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                                                               CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gorlach, Jorn
                                                             NAME/KEY:
                                                                                                                                                               Query Match
Best Local Similarity
Matches 81; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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Best Local Simil
Matches 39; (
                                                                                                                        US-09-909-207-28
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGAATTTGAAAAGATTGAGGCTGTTGTTTGTGATGTGTATTGGATTTGTGCTGACACTG 60
                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PATCHILD NA-DOS
SOFFWARE: PATCHILD NA-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99/909,207
FILING DATE: 19-Jul-2001
CLASSIFICATION NUMBER: 08/470,953
FILING DATE: 19-Jul-2001
PRIOR APPLICATION NUMBER: 08/470,953
FILING DATE: 06-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F: Gadiano. Esq.
REGISTRATION NUMBER: 37,136
REGISTRATION NUMBER: 37,136
TELERARION FOR GADIANO: 28:
TELERAX: (202) 293-1850
TELERAX: (50.3 293-1850
TELERAX: 650 383-5605
INFORMATION FOR SEQ ID NO: 28:
SERGURATION FOR SEQ ID NO: 28:
SERGURATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                         Length 81
                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                         1 ATGAATTTGAAAAGATTGAGGCTGTTGTTTTGTGATGTGTATTGGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSE: WILLIAN BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ANDREE LAHAYE
ERIC DE BUYL
PIERRE LEDOUX
RENE DETROZ
TITLE OF INVENTION: Xylanase, microorganisms
                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 81; DB 9; Sest Local Similarity 100.0%; Pred. No. 1.1e-17; Matches 81; Conservative 0; Mismatches 0;
REFERENCE/DOCKET NUMBER: 4121-40 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                    ;
TOPOLOGY: linear
;
MOLECULE TYPE: DNA (genomic)
;
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-,09-909-207-27
                             TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
. LENGTH: 81 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ACGCTGTGCCGCTCATGCG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 Accertarececertarece 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 28, Application US/09909207
Patent No. US20020115181A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 81 base pairs
                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington STATE: D.C.
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1219 Argcarctrarradaardadaardracaraardardarrahardgrirgrecrdadarrd 1278
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                                                                                                                                                                                                                                                                                                                                                                                                                                             problem in currention:

APPLICANT: Manage, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REPERENCE: 108827.128
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2000-04-30
FRIOR PILING DATE: 2000-07-18,066
FRIOR PILING DATE: 2000-07-29
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR PILING DATE: 2000-03-29
FRIOR PILING DATE: 2000-03-29
FRIOR PILING DATE: 1999-11-23
FRIOR APPLICATION NUMBER: US 60/185,218
FRIOR APPLICATION NUMBER: US 60/167,363
FRIOR PILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-09-24
FRIOR FILING DATE: 1999-09-24
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-38
FRIOR FILING DATE: 1999-09-38
                                                                                                                               1 ATGAATTTGAAAAGATTGAGGCTGTTGTTTTGTGATGTGTATTGGATTTGTGCTGACACTG
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                                                                                   Gaps
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 1080271.29
CURRENT APPLICATION NUMBER: US/10/027, 632
CURRENT FILING DATE: 2002-04-30
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                                   Length 2363;
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                                                                                   20; Indels
                                   Score 29; DB 13;
Pred. No. 15;
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                                                                                 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 263227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-027-632-263228
; Sequence 253228, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 263227, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:
                                           35.8%;
67.2%;
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Best Local Similarity 67.2%;
Matches 41; Conservative
                          Query Match
Best Local Similarity 67.2%
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US-10-027-632-263227
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US-10-027-632-263228
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APPLICANT: Warnillow:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REPERENCE: 108627.129
CURRENT APPLICATION NUMBER: US/10/027.632
CURRENT FILING DATE: 2002-04-30
FRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR APPLICATION NUMBER: US 60/185,218
FRIOR APPLICATION NUMBER: US 60/185,368
FRIOR APPLICATION NUMBER: US 60/167,363
FRIOR PILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-09-28
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  PPLICANT: Wang, David G.
ITLE OF INVENTION: Identification and Mapping of Single Nucleotide
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Pred. No. 15;
0; Mismatches
                                                                                                                                                       NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                        FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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; Sequence 253228, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
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Best Local Similarity 67.29
Matches 41; Conservative
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US-10-027-632-263227
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ORGANISM: Human
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LENGTH: 2363
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Pred. No. 15;
0; Mismatches 20; Indels
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| Sequence 97, Application US/10087192
| Publication No. US20020182586A1
| GENERAL INFORMATION:
| APPLICANT: MOTIS, David W. |
| APPLICANT: Engelhard, Eric K. |
| TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR |
| TITLE OF INVENTION: ACANCER |
| FILE REFERENCE: 529452000122 |
| CURRENT FILING DATE: 2002-03-01 |
| PRIOR PILING DATE: 2002-03-01 |
| PRIOR PAPLICATION NUMBER: US 09/747,377 |
| PRIOR PAPLICATION NUMBER: US 09/747,377 |
| PRIOR PAPLICATION NUMBER: US 09/798,586 |
| PRIOR PILING DATE: 2001-03-02 |
| NUMBER OF SEQ ID NOS: 2059 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| LENTH: DATE: DATE |
| LENTH: A333060 |
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    PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR PLING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-09
PRIOR PILING DATE: 1999-08-09
2000-07-12
MITMRER: US 60/198,676
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LCCATION: (1)...(233060)

CTHER INFORMATION: n = A,T,C or G

US-10-087-192-97
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Best Local Similarity 67.2%;
Matches 41; Conservative
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US-10-027-632-263228
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1 Similarity 63.2%; Pred. No. 1e+02;
43; Conservative 0; Mismatches 25; Indels 0:
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APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: CANCEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER
FILE REFERENCE: 5.2945.20001.2.
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT APPLICATION NUMBER: US/9/147,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR PELING DATE: 2000-13-02
NUMBER OF FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                        APPLICANT: More and W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER FILE REFERENCE: 529452000122
CURRENT PILLING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1615.
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Publication No. US20020182586A1
GENERAL INFORMATION:
Sequence 1615, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (1)...(72314)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 63.2%;
Matches 43; Conservative (
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US-10-087-192-1342
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Matches 43; Conserv
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61 ACGCCTGTG 69
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-437-963-16223/c
                                                                                                         US-10-425-115-83971/c
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Sequence 162687, Application US/10425115
Sequence 162687, Application No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: APPLI
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Sequence 137066, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Exou, Yihua
APPLICANT: Cao, Yongua
APPLICANT: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER: OF SEQ_ID NOS: 369326
70914 ATATGAAGGGCTGAGGCTAGTGTTTTGTCTTTTAAATAGATGAGTTCCCACTGTGTCTT 70855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 TGAAAAGATTGAGGCTGTTTGTGATGTGTATTGGATTTGTGCTGACACTGACGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 ATTIGAAAGAITGAGGCIGITGITTIGIGAIGIGIATIGGAT 46
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US-10-425-115-137066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , OTHER INFORMATION: Clone ID: MRT4577_79947C.1
US-10-425-115-162687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.8<sup>†</sup>
Matches 45; Conservative
                                                                                                                                                  70854 Criccicric 70847
                                                                              65 CTGTGCCG 72
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Best Local Similarity
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                               RESULT 11
US-10-425-115-162687/c
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LENGTH: 1383
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REPERENCE: 38-21(53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 16223
LENGTH: 648
Sequence 83971, Application US/10425115

Sequence 83971, Application US/10425115

Publication No. US20040214272A1

GRNERAL INFORMATION:

APPLICANT: La Royalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Choice Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21 (53222) B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 83971

LENGTH: 263
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33.8%; Score 27.4; DB 18; Length
Best Local Similarity 75.6%; Pred. No. 25;
Matches 34; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 TITGAAAAGAITGAGGCIGITGITIGIGAIGIGIATIGGAITIGI
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US-10-437-963-16223
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US-10-425-115-83971
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; Pred. No. 33;
0; Mismatches
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; Publication No. US20040123343A1
; GENERAL INFORMATION:
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Barbazuk, Brad
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Best Local Similarity 62.3%;
Matches 43; Conservative
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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RESULT 15
US-10-437-963-71944

Sequence 71944, Application US/10437963

FUBLication No. US200401233431

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: BLABERICON: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT PLING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 71944

LENGTH: 1763

FUBLICANT: Application NUMBER OF SEQ ID NOS: 204966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_72369C.1
US-10-437-963-71944
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ORGANISM: Oryza sativa
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Search completed: November 11, 2004, 02:08:35 Job time : 55.7881 secs

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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Bacillus
US-08-470-953A-1
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TYPE: nucleic acid
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Sequence 2, 7
Sequence 4, 7
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663
1 CAAATCGTCACCGACAATTC......TAACTTTGGATAAAAACAAT
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-08 470-953A-5
US-08 470-953A-5
US-08 470-953A-1
US-08 470-953A-1
US-08 470-953A-1
US-09-189-060B-1
US-08-501-126-18
US-09-603-311-23
US-09-603-311-23
US-09-603-311-23
US-09-603-311-23
US-09-603-311-23
US-09-075-526C-35
US-09-076-677-1
US-09-076-677-1
US-09-076-677-1
US-09-076-677-1
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US-09-076-677-1
US-09-076-677-1
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US-08-275-526C-32
US-09-076-677-30
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                     - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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RESULT 1

195-08-4706/533A-1

195-08-4706/533A-1

Sequence 1. #Pplication USA/08470953A

Patent No. 6346407

GENERAL NECREMATION

GENERAL NECREMATION

PAPLICANT: ENIC DE BITAL

APPLICANT: RIBE LAMAYE

APPLICANT: RIBE LAMAYE

APPLICANT: RIBE ELEGOUX

ADDRESS: 29

CORRESPONDENCE ADDRESS: 29

CORRESPONDENCE ADDRESS: 30

CORRESPONDENCE ADDRESS: 30

CORRESPONDENCE ADDRESS: 30

CONFERT: 2000 K St. N.W., Suite 200

CITY: Washington

STATE: D.C.

CONFITE: ISM PC Compatible

COMPUTER: ISM PC COMPATION: ADDRESS: ISM PC COMPATION: ADDRESS: ISM PC COMPATION: ADDRESS: ISM PC COMPATION: ADDRESS: ADD
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MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                 LENGTH: 663 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                    STRAIN: Bacillus
                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
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                   Length 663;
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100.0%; Pred. No. 7.9e-198;
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                             100.0%;
                                 Query Match 100.
Best Local Similarity 100.
Matches 663; Conservative
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Xylanase, microorganisms produced it, DNA molecule, processes for preparation of this xylanase and uses thereof 29 Sequence 2, Application US/08470953A

Sequence 2, Application US/08470953A

Patent No. 6346407

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: BRIC DE BUYL

APPLICANT: BRIC DE BUYL

APPLICANT: BRIC DE BUYL

APPLICANT: RENE DETROZ

TITLE OF INVENTION: Xylanase, micro

TITLE OF INVENTION: DNA molecule, promise of STREET: 2000 K St., N.W., Suite 2

STREET: 2000 K St., N.W., Suite 2

COUNTRY: U.S.A.

RESULT 2 US-08-470-953A-2

HOFER GILSON & LIONE Suite 200

360

240

300 381 420

480

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GENERAL INFORMATION:
APPLICANT: ANDREE LAHAYE
APPLICANT: ERIC DE BUYL
APPLICANT: PIERRE LEDOUX
APPLICANT: RENE DETROZ
TITLE OF INVENTION: Xylanase, microorganisms produced it,
TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase
TITLE OF INVENTION: and uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGGGGTACGTTCAGTGCCCAATGG 201
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                          CAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN E
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| Sequence 4, Application US/08470953A
| Sequence 4, Application US/08470953A
| Sequence 4, Application US/08410953A
| Sequence 6, Application Colored C
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                            Gaps
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100.0%; Score 663; DB 3; Length 744;
Best Local Similarity 100.0%; Pred. No. 8.4e-198;
Matches 663; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Flam PC-COMPATISh
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/470,953A
FILING DATE.—G-COTOBER-1995
FLOR APPLICATION DATA:
APPLICATION NUMBER: US/08/470,953A
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WITHLEMP Gadiano, ESQ.
REGISTRATION NUMBER: 37,136
REGISTRATION NUMBER: 37,136
REGISTRATION NUMBER: 37,136
REGISTRATION NUMBER: 202-429-0625
TELEFRAX: (2020) 293-1850
TELEFRAX: (520) 393-1850
TELEFRAX: (520) 393-1850
TELEFRAX: (520) 393-1850
TELEX: (520) 393-1850
TELEX: (530) 393-1605
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TYPE: nucleic acid
STRANDEDNESS: single
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Xylanase, microorganisms produced it,
DNA molecule, processes for preparation of this xylanase
and uses thereof
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Best Local Similarity 100.0%; Score 663; DB 3; Length 1
Best Local Similarity 100.0%; Pred. No. 1.2e-197;
Matches 663; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08470,953A
FILING DATE: 6-OCTOBER-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08470953A

Sequence 10, Application US/08470953A

Patent No. 6346407

GENERAL INFORMATION:
APPLICANT: ANDREE LAHAYE
APPLICANT: PIERRE LEDOUX
APPLICANT: PIERRE LEDOUX
TITLE OF INVENTION: Xylanaee, microorganisms produce
TITLE OF INVENTION: DNA molecule, processes for pref
TITLE OF INVENTION: and uses thereof
NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:
ADDRESSE:

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Wilhlem F. Gadiano, Esc
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 412:
TELECOMMUNICATION INFORMATION:
TELEPANONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1513 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STRAIN: Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 2000 K St
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGAACCATCACTGTTGATGGAGGA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            442 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACA 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 AACCACTTTAGAGCGTGGGAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCG 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATAGCGGTGGCTCTCTGGACAATGATTCTCAATCGTGGCGGTACGTTCAGTGCCCAATGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 AACAATGTTAACAACATATTATTCCGTAAAGGTAAAAATTCCAATGAAACACAAACACAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAACAAGIIGGIAACAIGTCCAIAAACIACGGAGCCAACIICCAACCAAAIGGIAAIGGG 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      382 IGGGGCAACTGGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGA
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                              Patentin Release #1.0, Version #1.25
                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,953A
FILING DATE: 6-OCTOBER-1995
                                                                                                          mat_peptide
82..744
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1..81
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NAME/KEY: CDS
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NAME/KEY:

LOCATION:
FEATURE:

NAME/KEY:

LOCATION:

LOCATION:

US-08-470-953A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         701 CAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTTTTGGAAA
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100.0%; Score 663; DB 3; 1
Best Local Similarity 100.0%; Pred. No. 1.2e-197;
Matches 663; Conservative 0; Mismatches 0;
                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, EEG.
REGISTRATION NUMBER: 37,136
REPERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 293-1850
TELEFAX: (202) 293-1850
TELEFAX: (302) 293-1850
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1513 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
              6-OCTOBER-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: mat peptide LOCATION: 701..1363
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LOCATION: 620..700
                FILING DATE: 6-OCTOR
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN: Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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MOLECULE TYPE: I
ORIGINAL SOURCE:
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US-08-470-953A-11
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NAME/KEY:
LOCATION:
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Patent No. 6446407

GENERAL INFORMATION:

APPLICANT: BANDRE LAHAYE

APPLICANT: RILE DE BUYL

APPLICANT: RILE BUYL

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701 CAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAA 760
                                             GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGG 120
                                                                     AACCACTITAGAGCGTGGGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCG
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 2000 K St. CITY: Washington STATE: D.C. COUNTRY: U.S.A.
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US-08-470-953A-11
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APPLICANT: Outtrup, Helle
APPLICANT: Outtrup, Helle
APPLICANT: Outtrup, Helle
APPLICANT: Dambmann, Claus
APPLICANT: Dambmann, Claus
APPLICANT: Olsen, Arne Agerlin
APPLICANT: Sch lein, Martin
APPLICANT: Sch lein, Martin
APPLICANT: Sch lein, Martin
APPLICANT: Olsensen, Per Linaa
TITLE OF INVENTION: DNA CONSTRUCTS AND METHODS OF PRODUCING
TITLE OF INVENTION: XYLANOLYTIC ENZYMES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 57704240 No. 5770424disk of No. 5770424th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STRATE: New York
STRATE: New York
STRATE: New York
STRATE: Roppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: BM PC compatible
ORPERATING SYSTEM: PC-DOS/MS-DOS
OOFFWARR: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                     562 AACCACTTTAGAGGGTGGGAAACTTAGGGATGAACATGGGGGAAAATGTATGAAGTCGCG 621
                                                                                                                                                                                                                  541 CITACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAATGTATATAGCAATACACTAAGA
                                                                                                                                                                                                                                                      481 AACCACTTTAGAGCGTGGGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCG
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APPLICATION NUMBER: US/08/698,978
FILING DATE: 16 August 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/470,398
FILING DATE: 06-JUN-1996
PRIOR APPLICATION NUMBER: 08/34,600
FILING DATE: 30-NOV-1994
PRIOR APPLICATION NUMBER: 08/34,600
FILING DATE: 2-JUL-92
APPLICATION NUMBER: PCT/DK93/00218
FILING DATE: 2-JUL-92
ATTORNEY/AGENT INFORMATION:
NAME: Greegy, Valeta A.
REGISTRATION NUMBER: 35,127
REGISTRATION NUMBER: 35,127
REGISTRATION NUMBER: 35,127
REGISTRATION NUMBER: 35,127
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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GENERAL INFORMATION:
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                                                                                   TATTTATGCGTCTATGGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGT 300
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                                               541 CITACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAATGTATATAGCAATACACTAAGA 600
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Sequence 1, Application US/09189060B

Patent No. 6270968

GENERAL INFORMATION:
APPLICANT: Dalboge, Henrik
APPLICANT: Sandal, Thomas

APPLICANT: Rauppinen, Markus
TITLE OF INVENTION: Method Of Providing No. 6270968el DNA Sequences

TITLE OF INVENTION: Lidericheen
TITLE OF INVENTION: WUMBER: US/09/189,060B

CURRENT RILING DATE: 1999-10-10

PRIOR PILING DATE: 1999-705-12

NUMBER OF SEQ ID NOS: 74

SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 8.9e-189;
0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 95.7%;
Best Local Similarity 97.3%;
Matches 645; Conservative
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US-09-189-060B-1
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LOCATION: (1)
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US-09-189-060B-1
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LENGTH: 744
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121 AACAATGTTAACAACATATTATTCCGTAAAGGTAAAAATTCAATGAAACACAAAACACAC 180
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                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,126
FILING DATE: 29-DEC-1995
CLASSIFICATION: 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.2%; Score 624.6; DB 3;
96.4%; Pred. No. 9.1e-186;
tive 0; Mismatches 24;
APPLICANT: Van Beckhoven W.C., Rudolf F. APPLICANT: Quax, Wilhelmus J. APPLICANT: Quax, Wilhelmus J. TITLE OF INVENTION: ALKALI-TOLERANT XYLANASES NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 1..744
CTHER INFORMATION: /product= "xylanase"
US-08-501-126-18
                                                                                                                                 ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CBS672.93
                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Murashige Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4615
TELECOMMUNICATION INFORMATION:
TELEFRONE: (202) 887-1500
TELEFRAX: (202) 887-1500
TELEFRAX: (202) 887-1500
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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TYPE: nucleic acid
STRANDEDNESS: double
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INDIVIDUAL ISOLATE:
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Best Local Similarity
Matches 639; Conserval
                                                                                                                                                                  CITY: Washington
STATE: DC
COUNTRY: USA
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                                                                                                                                                                        Length 871;
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                                                                                                                                                                      Score 634.2; DB 1;
Pred. No. 9.7e-189;
0; Mismatches 18;
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Van Der Kleij, Wilhelmus A.
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Williams, Diane P.
Iverson, Sara
Farrell, Roberta L.
                                           agaradherens
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Patent No. 6140095
GENERAL INFORMATION:
APPLICANT: Van Solingen, Pieter
                                                                                                                                                                        Query Match 95.7%;
Best Local Similarity 97.3%;
Matches 645; Conservative
                                            ORGANISM: Bacillus a
                                                                                                   CDS
82..744
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                             ORIGINAL SOURCE:
                                                                                               , NAME/KEY:
, LOCATION:
US-08-698-978-1
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APPLICANT:
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Length 744; Indels 240

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TYPE: DNA ORGANISM: Clostridium stercorarium
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US-09-390-234-23
Sequence 23, Application US/09390234
Patent No. 6365390
GENERAL INFORMATION:
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; NAME/KEY: CDS
; LOCATION: (440)..(1975)
US-09-390-234-23
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                  CTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAATGTATATAGCAATACACTAAGA 600
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                                                                                                                                                                                                                                                                                             Sequence 11, Application US/09189060B

Sequence 11, Application US/09189060B

Betent No. 6270968

GENERAL INFORMATION:
APPLICANT: Balboge, Henrik
APPLICANT: Banboge, Henrik
APPLICANT: Barge, Diderichsen
TITLE OF INVENTION: Markus
FILE REPERENCE: 4772.204-03
FILE REPERENCE: 4772.204-03
FURENT APPLICATION NUMBER: US/09/189,060B
CURRENT FILING DATE: 1998-11-10
PRIOR PILING DATE: 1997-05-12
NUMBER: O SEQ ID NOS: 74
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAAATTTTGGAAA
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                                                           TITAAACAATAITIGGAGTGITCGAAGAICGAAACGCACGAGGGGCACGAITICIGIGGC
                                                                        Gaps
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US-09-189-060B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
                                                                                                                                                                                                                                                                                  RESULT 10
US-09-189-060B-11
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APPLICANT: Blum, David L.
APPLICANT: Blum, David L.
APPLICANT: Li, Xin-Liang
APPLICANTON: Phenolic Acid Esterases, Coding Sequences and Methods
FILE REFERENCE: 7-98
CURRENT FILING DATE: 1999-09-03
EARLIER APPLICATION NUMBER: US 60/099,136
EARLIER APPLICANTON NUMBER: US 60/099,136
SEQID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQID NO 224
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TATTIGIGIGITIACGGTIGGACAAGAAATCCACIGGTIGAATATTACATIGIAGAAAGC 829
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GATAGCGGTGGCTCTGGGACAATGATTCTCAATGGCGGTACGTTCAGTGCCCAATGG
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                                     GA---CTACGGAAATACGATTATGGAACTTAACGACGGTGGTACTTTTAGTTGTTGTATGG
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200
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COMPUTER READABLE FORM:
COMPUTER: READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/275,526C
FILING DATE: 15-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WILLIAN BRINKS HOFER
00 K St., N.W., Suite
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APPLICANT: DE BUY
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APPLICANT: Li, Xin-Liang
APPLICANT: Li, Xin-Liang
APPLICANT: Li, Xin-Liang
APPLICANT: Azain, Michael J.
APPLICANT: Azain, Michael J.
APPLICANT: Blum, David L.
APPLICANT: Blum, David L.
APPLICANT: Rataeva, Irina
TITILE OF INVENTION: Phenolic Acid Esterases, Coding Sequences and Methods
FILE REFERENCE: 67-98A
CURRENT FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: US/09/603,311
CURRENT FILING DATE: 1998-09-04
PRIOR FILING DATE: 1998-09-04
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
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                                                                  GGAACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCC 417
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                                                                                                             TATTIATGCGTCTATGGTTGGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGT
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0; Mismatches 206;
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Patent No. 6602700
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Best Local Similarity 65.6
Matches 405; Conservative
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; LOCATION: (440)..(1975)
US-09-603-311-23
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LENGTH: 2364
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US-09-603-311-23
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XYLANASE DERIVED FROM A BACILLUS SPECIES,
EXPRESSION VECTORS FOR SUCH XYLANASE AND
OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
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ADDRESSER: WILLIAN BRINKS HOFER GILSON & LIONE, P.C. STREET: 2000 K St., N.W., Suite 200
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/275,526C
FILING DATE: 15-JUL-1994
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ATORNEY AGENT INFORMATION:
NAME: Gadiano, Wilhlem F.
REGISTRATION NUMBER: 37,136
REFRENCE/DOCKET NUMBER: 4121-49
TELEPHONE: (202) 429-0625
TELEFAX: (202) 299-0625
TELEX: 650 383 5605
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
REDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                       APPLICANT: LAHAYE, ANDR E
APPLICANT: LEDOUX, PIERRE
APPLICANT: AMORY, ANTOINE
APPLICANT: AMORY, REN
APPLICANT: VETTER, ROMAN
TITLE OF INVENTION: XYLANASE DEI
TITLE OF INVENTION: CYTHER PROTEI
TITLE OF INVENTION: OTHER PROTEI
TITLE OF INVENTION: OTHER PROTEI
TITLE OF INVENTION: USE THEREOF
NUMBER OF SEQUENCES: 35
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MOLECULE TYPE: genomic DNA
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Best Local Similarity 65.55
Matches 406; Conservative
                          APPLICANT: DE BUYL, ERIC
APPLICANT: LAHAYE, ANDR
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STRANDEDNESS: single
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COUNTRY: U.S.A.
ZIP: 20006
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US-08-275-526C-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 38.5%; Score 255.2; DB 3; Length Best Local Similarity 65.5%; Pred. No. 5.9e-70; Matches 406; Conservative 0; Mismatches 208; Indels
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ATTORNEY AGENT INFORMATION:
NAME: Gadiano, Wilhlem F.
REGISTRATION UNDRER: 37,131-
REFERENCE/DOCKET UNDRER: 4121-
TELECOMMUNICATION INFORMATION:
TELEFRAK: (202) 293-0625
TELEFAK: (202) 293-0625
TELEFAK: 650 383 5605
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1022 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
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STRAIN:
US-08-275-526C-1
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Length 1022;
38.5%; Score 255.2; DB 3;
65.5%; Pred. No. 5.9e-70;
iive 0; Mismatches 208;
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; Sequence 35, Application US/08275526C

RESULT 14 US-08-275-526C-35

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MOLECULE TYPE: genomic DNA ORIGINAL SOURCE:
                                                                                                          Query Match
Best Local Similarity 65.5%;
Matches 406; Conservative
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      576 CGTCCAACAGG---AACGTATAAAGGATCATTTTATGCCGATGGAGGCACATATGACATA 632
                                                                                               TGGAGTGTTCGAAGATCGAAACGCACGAGGCACGATTTCTGTCAGCAACCACTTTAGA 492
                                                                                                                                                           493 GCGTGGGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCGCTTACTGTAGAA
                                                                                                                                                                                     753 AAATGGGAAAGCTTAGGCATGCCAATGGGAAAAATGTATGAAACAGCATTAACTGTAGAA
                                                                                                                TACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATTTAAACAATAT
                                                              633 TATGAAACGCTCCGTGTCAATCAGCCTTCTATCATTGGAGACGCTACCTTCAAACAATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXPRESSION VECTORS FOR SUCH XYLANAGE AND OTHER PROTEINS, HOST ORGANISMS THEREFOR AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE: 12-May-1998
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION DATA:
APPLICATION NUMBER: US 08/275,526
TILING DATE: 15-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Gaddiano, Wilhlem F.
REGISTRATION NUMBER: 37, 136
REFERENCE/DOCKET NUMBER: 4121-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INVENTION: XYLANASE DERIVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-0625
TELEX: 650 383 5605
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMORY, ANTOINE
DETROZ, RENE
ANDRE, CHRISTOPHE
VETTER, ROMAN
                                                                                                                                                                                                                                                                                   CCTCTCTCAACTATTAGTAA 632
                                                                                                                                                                                                                                                                                                               CATATGAAAAAGCCAGCAA 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1022 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09076677
Patent No. 6423523
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DE BUYL, ERIC
LAHAYE, ANDREE
LEDOUX, PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D.C. COUNTRY: U.S.A. ZIP: 20006
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                                                                                                                                                        Length 1022;
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                                                                                                                                                        DB 4;
                                                                                                                                                   Score 255.2; DB 4;
Pred. No. 5.9e-70;
0; Mismatches 208;
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ne : 79.1638 secs
ORGANISM: Bacillus pumilus
STRAIN: PRL B12
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-076-677-1
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November 10, 2004, 15:55:17 ; Search time 420.566 Seconds (without alignments) 8275.436 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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663
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description			Aat16103 Xylanase	Aav13067 Glycosyl	Aav30255 DNA encod	Aaq92878 Thermosta	Aav13074 Xylanase	Adj34947 DNA encod	Adj35051 DNA encod	Aaz51821 Clostridi	Aag80923 B. pumilu	Adj34969 DNA encod	Aat90972 Nucleotid	~	Adj35011 DNA encod	Aaq92876 Thermosta	Aaq92875 Thermosta	Adj35101 DNA encod			Adj34999 DNA encod
SUMMARIES	a	AAT16101	AAT16102	AAT16103	AAV13067	AAV30255	AAQ92878	AAV13074	2 ADJ34947	2 ADJ35051	AAZ51821	AAQ80923	2 ADJ34969	AAT90972	AAT08142	2 ADJ35011	AAQ92876	AAQ92875	2 ADJ35101	2 ADJ35151	2 ADJ34965	2 ADJ34999
	Length DB	663 2	744 2	1513 2	744 2	871 2	744 2	747 2	1068 13	1956 13	2364 3	1022 2	684 13	1190 2	1244 2	747 13	164 2	164 2	1695 13	1338 13	1077 13	1065 13
	* Query Match L	100.0	100.0	100.0	95.7	95.7	94.2	76.6	56.0	41.7	38.5	38.5	38.5	32.0	30.9	26.8	23.3	22.8	21.7	21.3	20.5	19.6
	Score	663	663	663	634.2	634.2	624.6	507.8	371.2	276.4	255.4	255.2	255	212.2	204.8	177.8	154.4	151.2	143.6	141.2	136.2	130.2
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128.4 121.2 119.4 119.4	119.4 117.8 117.6 116.8 115.2 115.2	115.2 111.1 111.2 111.1 111.4 1110.8 110.8
22 23 24 25	0 2 2 8 8 2 7 6 8 8 4 8 8 8 4 8 8 8 8 8 8 8 8 8 8 8 8	0 19 19 19 19 19 19 19 19 19 19 19 19 19 1

ALIGNMENTS

Applicant's down Xylanase; thermostable enzyme; paper; pulp; bleaching; feedstuff; baking; Detroz R; Bacillus sp; strain 710/1 (LMG P-14798): 1. .663 /*tag= a /EC_number= "3.2.1.8" Location/Qualifiers Ledoux P, AAT16101 standard; DNA; 663 BP 95AU-00025086. 94BE-00000706. (revised)
(first entry) De Buyl E, Lahaye A, (SOLVA) SOLVAY SA. Xylanase gene. 26-JUL-1994; 17-MAY-1995; 16-OCT-2003 15-MAY-1996 ,2601-1111-0mat_peptide AU9525086-A 08-FEB-1996 AAT16101; RESULT 1

Bacillus derived xylanase active over wide pH range - used in treatment of paper pulp, animal feeds and in bakery goods. WPI; 1996-117341/13. P-PSDB; AAR92053.

Claim 30; Page 50-51; 94pp; English.

A DNA sequence (AAT16101) coding for a thermostable mature xylanase (AAR92053) was isolated from a gene library of Bacillus sp. 720/1 (LMG P-

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14798). Sequences were also obtd. (see AAT16102 and AAT16103) for the xylanase precursor and for the complete gene including 5' and 3' untranslated sequences. DNA coding for the mature enzyme may be incorporated into a vector and expressed from either its own promoter or from the Bacillus pumilus PLB 12 promoter (AAQ73996), and used for prodn. of recombinant xylanase in transformed hosts, pref. Bacillus licheniformis or B. pumilus. The enzyme is useful in the paper-pulp, animal feed and baking industries. (Updated on 16-OCT-2003 to standardise OS field)
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                                                                                                                                                                       Length 663;
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5e-188;
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Pred. No. 5
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100.0%;
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180 A DNA sequence (AAT16102) coding for a xylanase precursor (AAR92054) was isolated from a gene library of Bacillus sp. 720/1 (LMG P-14798). The sequence (AAT16103) for the complete gene including 5' and 3' untranslated sequences was also obtd. The gene may be incorporated into a vector and expressed from either its own promoter or from the Bacillus pumilus PRL B12 promoter (see AAQ73956), and used for proof. of recombinant thermostable xylanase in transformed hosts, pref. Bacillus licheniformis or B. pumilus. The enzyme is useful in the paper-pulp, and mal feed and baking industries. (Updated on 16-OCT-2003 to standardise 120 261 240. 321 141 201 9 Xylanase; thermostable enzyme; paper; pulp; bleaching; feedstuff; baking; treatment GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGG **AACAATGTTAACAACATATTATTCCGTAAAAGGTAAAAAATTCAATGAAACACAAACACA** CAAATCGTCACCGACAATTCCCATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAA Gaps ö used in Length 744; Sequence 744 BP; 246 A; 144 C; 160 G; 194 T; 0 U; 0 Other; Indels 1 wide pH range cery goods. 100.0%; Score 663; DB 2; L ilarity 100.0%; Pred. No. 5.3e-188; Conservative 0; Mismatches 0; 3 derived xylanase active over wide pulp, animal feeds and in bakery Detroz strain 710/1 (LMG P-14798) "3.2.1.8" Location/Qualifiers Claim 9; Page 54-55; 94pp; English Ledoux P, 94BE-00000706. 95AU-00025086 number= Bacillus derived xylanase 82. 744 /*tag= b Xylanase precursor gene 1. .81 /*tag= Lahaye A, WPI; 1996-117341/13. P-PSDB; AAR92054. /EC Similarity (SOLV) SOLVAY SA. Bacillus sp; 19-JUL-1995; 26-JUL-1994; 17-MAY-1995; ei ei 663; sig_peptide AU9525086-A 08-FEB-1996 mat_peptide 202 262 Н 82 61 121 181 paper Query Match Buyl Local Best Loca Matches g D oŧ g ò g ò g ò 셤 8

300

TTGTCGAATATTATATTGTCGACAGT

TATTTATGCGTCTATGGTTGGACTGTTGACCCTC

241

8 8

BP.

DNA;

AAT16102 standard;

RESULT 2 AAT16102 (revised)
(first entry)

16-OCT-2003 15-MAY-1996

SXEE

AAT16102;

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Gaps

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us-09-909-207-1.rng

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GATAGCGGTGGCTCTGGGACAATGATTCTCCAATGGCGGTACGTTCAGTGCCCAATGG 120
                                                                                                                                                                                                                                                               AACAATGTTAACAACATATTATTCCGTAAAGGTAAAAATTCAATGAAACACAAAACACAC
                                                  precursor (AAR92054) was
                                               A DNA sequence (AAT16102) coding for a xylanase precursor (AAR92054) wa isolated from a gene library of Bacillus sp. 720/1 (LMG P-14798). The gene may be incorporated into a vector and expressed in transformed hosts, pref. Bacillus licheniformis or Bacillus pumilus, for prodn. of thermostable mature xylanase (AAR92053). The enzyme is useful in the paper pulp, animal feed and baking industries. (Updated on 16-OCT-2003 standardise OS field)
    range - used in treatment
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                                                                                                                                                                                     CAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTT
                                                                                                                                                Length 1513;
                                                                                                                             Sequence 1513 BP; 500 A; 282 C; 271 G; 460 T; 0 U; 0 Other;
                                                                                                                                                                 0; Indels
                                                                                                                                                100.0%; Score 663; DB 2; I 100.0%; Pred. No. 7.1e-188; ive 0; Mismatches 0;
     Bacillus derived xylanase active over wide pH ra
of paper pulp, animal feeds and in bakery goods
                                 Claim 10; Page 59-61; 94pp; English.
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                                                                                   TGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGAACCATCACTGTTGATGGAGGA
                                    ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACA
                                               TTTAAACAATATTGGAGTGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGC
                                                                                                              AACCACTTTAGAGCGTGGGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCG
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95BE-00000448
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P-PSDB; AAR92054.
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17-MAY-1995;
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15-MAY-1996
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561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xylanolytic enzyme; Bacillus agaradherens NCIMB 40482; breakdown; agricultural waste; alcohol fuel; enzymatic treatment; animal feed; release; free pentose sugar; dissolving pulp; cellulose; bio-bleaching; wood pulp; lignocellulostic material; animal feed additive; ss.
                                                                                                                             382 TGGGGCAACTGGCGTCCACCAGGGGCAACGCCTAAGGGAACCATCACTGTTGATGGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                              601 ATTAACGGTAACCTCTCTCAACTATTAGTAATGACGAGAGCGTAACTTTGGATAAAAAC
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82. .747
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94US-00343600.
95US-00470398.
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Jorgensen PL, Dambmann C;
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P-PSDB; AAW60562.
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06-JUN-1995;
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(i) PCR amplification of the DNA with PCR primers with homology to (a) known gene(s) encoding a polypeptide with an activity of interest; (ii) linking the obtained PCR product of a 5' structural gene sequence and a 3' structural gene sequence and a sequence; (iiv) screening for hybrid DNA sequences encoding a polypeptide with the activity of interest or a related activity; and (v) isolating the hybrid DNA sequence identified in step (iv). This method provides for identification and isolation of sequences from microorganisms without having to cultivate and isolate the microorganism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 CAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAA
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                                                                                                                                                                                                                                                                                                Glycosyl hydrolase family 11 xylanase DNA derived from Bacillus
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                                                                                                                                                              Bacillus sp; xylanase; glycosyl hydrolase family 11; isolation; microorganism; identification; ss.
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Pred. No. 2.2e-179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 95.7%; Score 634.2; Best Local Similarity 97.3%; Pred. No. 2.2e Matches 645; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sandal T,
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                                                                 (first entry)
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P-PSDB; AAW44262.
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                                                                 19-MAY-1998
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                                                                                             The present sequence encodes a xylanolytic enzyme of Bacillus agaradherens NCIMB 40482. Xylanolytic enzymes are used for enzymatic breakdown of agricultural wastes for production of alcohol fuels, enzymatic treatment of animal feeds to release free pentose sugars, manufacturing of dissolving pulps yielding cellulose and bio-bleaching of wood pulp. They are also used for treatment of lignocellulostic material e0.3 peor and pulp, or as an animal feed additive. (Updaced on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS field.) (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                       Gaps
        construct encoding Bacillus agaradherens xylanolytic enzyme - and ors and Bacillus cells containing these, useful for recombinant luction of the enzyme for use in agricultural waste breakdown and
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                                                                                                                                                                                                                                                                              Length 871;
                                                                                                                                                                                                                                               Sequence 871 BP; 283 A; 171 C; 179 G; 238 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                          Match 95.7%; Score 634.2; DB 2; Local Similarity 97.3%; Pred. No. 2.4e-179; les 645; Conservative 0; Mismatches 18;
                                                 lignocellulostic material treatment
                                                                           Claim 1; Col 11-14; 10pp; English.
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                                     production of
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Matches 645
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The sequence encodes an alkaline endo-1,4-beta-D-xylanase (G-type) from Bacillus sp. 1-43-3. Fragments of the sequence (e.g. the internal fragments given in AAQ22876 and AAQ92877) may be amplified by polymerase chain reaction, e.g. using primers with sequences AAQ92866, AAQ92869. The DNA may be cloned in Escherichia coli using a plasmid vector for recombinant xylanase production. The xylanase may be used in the paper and pulp industries, where it produces an increase in treated pulp in an BCF pulp bleaching process, at pH 9.0 and 65 deg C. The enzyme may be used in production of paper, board and fluff pulp, and has low cellulase activity. The increased brightness produced using the xylanase allows reduction in the amount of bleaching chemicals used.
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                                                                                                                                                     pulp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel xylanase enzyme active at high p_{\rm H} - useful in paper and pulp processes.
                                                                                                                                                                                                                                                                                                                                                                          Herbes WT;
                                                                                                                                thermostable alkaline endo-1,4-beta-D-xylanase gene; cloning; polymerase chain reaction; Escherichia coli; EC-3.2.1.8; paper; bleaching; ds.
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, Van Beckhoven RFWC,
                                                                                                           Thermostable alkaline endo-1,4-beta-D-xylanase gene
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94.2%; Score 624.6; DB 2;
Best Local Similarity 96.4%; Pred. No. 1.7e-176;
Matches 639; Conservative 0; Mismatches 24;
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                                                                                                                                                                                                                                                                                                                                                                  , "LLIJams DP, Iver
; WA, Herweijer MA, V
', Jones BE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 42-43; 54pp; English.
                                                                                                                                                                                                 Bacillus sp; 1-43-3 (CBS 672.93)
          BP.
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          744
                                                                  (revised)
(first entry)
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          DNA;
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                                                                                                                                                                                                                                                                                                                                                                           Van Solingen P,
Van Der Kleij WA
Goedegebuur F,
                                                                                                                                                                                                                                                                                        23-DEC-1994;
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                                                                  16-OCT-2003
12-FEB-1996
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                                   The present sequence represents a positive clone for xylanase activity from an example of the present invention. The present invention describes a novel method for providing a novel DNA sequence encoding a polypeptide from a microorganism with an activity of interest. The method comprises: (1) PCR amplification of the DNA with PCR primers with homology to (a) known gene(s) encoding a polypeptide with an activity of interest; (ii) linking the obtained PCR product of a 5' structural gene sequence along a polypeptide with a sequence senceding a polypeptide with the activity of interest or a related activity; and (v) isolating the hybrid DNA sequence and (v) isolating the hybrid DNA sequence identified in step (iv). This method provides for identification and isolation of sequences from microorganisms without having to cultivate and isolate the microorganism
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                                                                                                                                                                                                                                                                         Length 747;
                                                                                                                                                                                                                                            Sequence 747 BP; 236 A; 168 C; 154 G; 189 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                        Query Match 76.6%; Score 507.8; DB 2; Best Local Similarity 85.4%; Pred. No. 1.6e-141; Matches 566; Conservative 0; Mismatches 97;
               Example 1; Page 35; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    663
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                                                                                                                              TGGGCCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGAACCATCACTGTTGATGGAGGA
                                                                                                                                                             ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolating novel DNA sequences from microorganisms - without the culturing the microorganism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          xylanase; glycosyl hydrolase family 11; isolation; m; identification; hybrid DNA; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xylanase activity positive clone DNA SEQ ID NO:11
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1. .747
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microorganism;
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Bacillus sp
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420

360 435 480

555 540 615

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The invention describes an isolated or recombinant polypeptide (I), having 50% or more identity to 190 300-1200 residue amino acid sequences (SI), given in the specification, over a region of 100 or more residues and the polypeptide as thermostable xylanase activity. (I) is useful for: dough conditioning; beverage production; as a nutritional supplement in
                                                                                                                                                                     acgrardacartrardacacacrecerercaceaceacerrecarradadecaceacea
                                                                                                                                                                                                                                                                                                                                                  CTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAATGTATATAGCAATACACTAAGA 600
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                         ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACA
                                                                                                                                                                                                          TTTAAACAATATTGGAGTGTTCGAAGATCGAAACGCACGAGGGCACGATTTCTGTCAGC
                                                                                                                                                                                                                                  AACCACTTTAGAGCGTGGGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-APR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes an isolated or recombinant polypeptide (I), having 50% or more identity to 190 300-1200 residue amino acid sequences (S1), given in the specification, over a region of 100 or more residues and the polypeptide as thermostable xylanase activity. (I) is useful for: dough conditioning, beverage production, as a nutritional supplement in animal feed; reducing lignin in a wood or a wood product; and for eliminating and protecting animals from a microorganism comprising xylan. The polynucleotide (II) encoding (I) is useful for amplifying nucleic acid encoding a polypeptide having a xylanase activity which involves amplifying (II) or its subsequence. (I) is useful for treating and preventing bacterial infection and fungal infection e.g. coccidiosis. This sequence encodes xylanase protein isolated from an environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cagacgarcaccaactarcercegracecardacecrrardacrardaracresaag 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGG 120
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                                                                                                                                                            dough conditioning; beverage production; nutritional supplement; animal feed; lignin reduction; wood product; xylan; bacterial infection; fungal infection; coccidiosis; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1068;
                                                                                                          DNA encoding xylanase from an environmental sample seq id 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 371.2; DB 12; Length
Pred. No. 1.5e-100;
0; Mismatches 138; Indels
                                                                                                                                               antibacterial; fungicide; thermostable xylanase activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         texture, treating paper, eliminating microorganisms.
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       standard; DNA; 1068 BP
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76.8%;
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                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Callen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-099016/10.
P-PSDB; ADJ34948.
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Esteghlalian A;
                                                                                                                                                                                                                                     Unidentified.
                                                                             22-APR-2004
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       ADJ34947
                                        ADJ34947;
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ઠ 셤 ò 요 ò 요 ઠ paper and pulp industry; feed processing; food additive; cell wall material; degradation; ds.

Ā

"Xylanase

/*tag= e /product= ' 440. .1978

WO200014243-A1

Location/Qualifiers

Key

Clostridium stercorarium

plant

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Ljungdahl

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Kataeva I, 2000-256991/22 P-PSDB; AAY70523

3lum DL,

UNIV GEORGIA RES FOUND INC

98US-0099136P 99WO-US020304

03-SEP-1999; 04-SEP-1998;

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                                                                                                                                                                                                                                                                                                                                         153
                                                                                                                                                                                                                                                                                                                                                                                                                                                        121. AACAATGTTAACAACATATTATTCCGTAAAGGTAAAAATTCAATGAAACACAAACACAC 180
 animal feed, reducing lignin in a wood or a wood product; and for calminating and protecting animals from a microorganism comprising xylan. The polynucleotide (II) encoding (I) is useful for amplifying nucleic acid encoding a polypeptide having a xylanase activity which involves amplification of a template nucleic acid with a primer pair capable of amplification of a template nucleic acid with a primer pair capable of preventing (II) or its subsequence. (I) is useful for treating and preventing bacterial infection and fungal infection e.g. coccidiosis. This sequence encodes xylanase protein isolated from an environmental
                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAACATTITIAAACAGTGGGAAAGAATGGGCATGCGAATGGGTAAGATGTATGAAGTTGCT
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                                                                                                                                                                                                                                                                                                      CAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTTTTGGAAA
                                                                                                                                                                                                                                                                    Gaps
reducing lignin in a wood or a wood product; and for
                                                                                                                                                                                                                                                                  <u>ب</u>
                                                                                                                                                                                                                               Length 1956;
                                                                                                                                                                                       Sequence 1956 BP; 614 A; 384 C; 423 G; 535 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                               DB 12;
                                                                                                                                                                                                                           Score 276.4; DB 12;
Pred. No. 4.9e-72;
); Mismatches 201;
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66.8%;
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The present sequence is a DNA encoding xylanase A (XynA) from Clostridium stercorarium. XynA contains family VI cellulose binding domain (CED) which is homologous to the CBD of xylanase Z (XynZ) of Clostridium thermocellum. XynZ is an enzymatic component of C. thermocellum cellulosome and has a multi-domain structure which includes a dockerin domain, a catalytic xylanase domain, a family VI cellulose binding domain and a domain of unknown function. The unknown domain in the N-terminal region of XynZ has been found to contain feruloy! (phenolic acid) esterase which is involved in the degradation of plant cell wall material. The novel feruloyl esterase is thermostable, easy to purify, has high temperature optima and stable over a wide pH range. The enzyme is used for producing ferulic acid from wheat bran or agricultural byproducts, treating grasses or other plant materials used in the pulp
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                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant DNA molecule comprising a sequence encoding feruloyl esterase protein, useful for treating grasses and other plant materials used in pulp and paper industries, feed processing and food additives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAACAAGITGGTAACAIGTCCAIAAACTACGGAGCCAACTTCCAACCAAATGGTAATGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          grasses or other plant materials used in tlend feed processing and as a food additive
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nes 405; Conservative
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Xylanase A; XynA; cellulosome; feruloyl esterase; phenolic acid esterase; thermostable; ferulic acid; wheat bran; agricultural byproduct; treat;

stercorarium xylanase A DNA.

Clostridium 04-JUL-2000

(first entry)-

BP

AAZ51821 standard; DNA; 2364

AAZ51821

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transformed Bacillus licheniformis, and related DNA, vectors, etc., used for pre-treatment of wood pulp to reduce chlorine or ozone consumption in subsequent bleaching.
                                    Claim 13; Fig 1a-1b; 97pp; English.
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                                                                                                                           38.5%;
65.5%;
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                                                                                                                                             Matches 406; Conservative
                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                   /*tag= b
/note= "base n at position 107 is not identified in the specification"
186. 1869 - /*tag= c
|186. .266
 890 GGTACTTATGAAATATATGAAACTACCCGGGTAAATCAGCCTTCCATCGATGGAACTGCG
                                                                                                  478 AGCAACCACTTTAGAGCGTGGGAAAACTTAGGGATGAATATGGGGAAAAATGTATGAAGTC
                              GGAACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCC
                                                                ACATITIAAACAATATIGGAGIGTICGAAGATCGAAACGCACGAGIGGCACGATITICIGIC
                                                                                                                                                                                                                                                                                                           Xylanase; endo-1,4-beta-D-xylanase; wood pulp; pulping; biobleaching; bleaching; bleaching; bleaching;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Purified xylanase from Bacillus pumilus PRL B12 - esp. produced in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ledoux
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lahaye A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detroz R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /EC_number= "3.2.1.8"
/note= "claim 10"
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267..866

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             М
                                                                                                                                                                         AGAATTAACGGTAACCC 614
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                                                                                                                                                                                                                                       standard; DNA; 1022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Buyl
                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                            B. pumilus xylanase gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SOLV ) SOLVAY & CIE
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                                                                                                                                                                                                                                                                                                                                       Bacillus pumilus
                                                                                                                                                                                                                                                                                                                                                                                          misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1993;
                                                                                                                                                                                                                                                                          02-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GB2279955-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                sig_peptide
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5'UTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATTTAAACAATAT 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATGCCTTATTTCGAAAAGGAAGTTTGATTCCACTAAAACTCATCATCAACTTGGC 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             515
                                                                                                                                                                                                                                                                                                                                               73 TCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGGAACAATGTTAAC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATACCTCGATGACACTCAATAACGGCGGGCATTTAGTGCAAGCTGGAACAATATTGGA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATEGITEGACTETTGACCCTCTTGTCGAATATTATATTGTCGACAGTTGGGGCAACTGG 312
                          recombinant plasmids carrying the xylanase gane. A chromosomal fragment obtained from isolate pBPX1 was subcloned and expressed in Escherichia coli JM109. The sequence of the xylanase gene (as a 1022 bp Sau3A1 fragment) carried by a selected transformant is given in AAQ80923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACATGTCCATAAACTACGGAGCCAACTTCCAACCAAATGGTAATGCGTATTTATGCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        516 TATGGCTGGACAATCTCCATTAGCTGAATACTACATTGTTGAGTCATGGGGGCACATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGAACATATGATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGAGTGTTCGAAGATCGAAACGCACGAGGCACGATTTCTGTCAGCAACCACTTTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     493 GCGTGGGAAAACTTAGGGATGAATATGGGGGAAAATGTATGAAGTCGCGCGCTTACTGTAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCTATCAAAGTAGCGGAAGTGCTAATGTATATAGCAATACACTAAGAATTAACGGTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACATATTATTCCGTAAAAGGTAAAAATTCAATGAAACACAAAACACAACAAGTTGGT
       for
                                                                                                                                                                                                                                                                                                      GACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAAGATAGCGGTGGC
                                                                                                                                                                                                                                                         Gaps
pumilus PTL B12 (ATCC 55443) gene library was screened
                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding xylanase from an environmental sample seq id 185.
                                                                                                                                                                                                        DB 2; Length 1022;
                                                                                                                                                    Sequence 1022 BP; 329 A; 197 C; 229 G; 266 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                     Score 255.2; DB 2;
Pred. No. 8.4e-66;
0; Mismatches 208;
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The invention describes an isolated or recombinant polypeptide (I), having 50% or more identity to 190 300-1200 residue amino acid sequences (S1), given in the specification, over a region of 100 or more residues and the polypeptide as thermostable xylanase activity. (I) is useful for: dough conditioning, beverage production, as a nutritional supplement in animal feed, reducing lignin in a wood or a wood product, and for eliminating and protecting animals from a microorganism comprising xylan. The polymucleotide (II) encoding (I) is useful for amplifying nucleic acid encoding a polypeptide having a xylanase activity which involves amplifying (II) or its subsequence. (I) is useful for treating and preventing bacterial infection and fungal infection e.g. coccidiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 GATAATAGGATAGGACACACAGGGATACGATTTTGAATTATGGAAGGATTAC---GGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGGAACAATGTTAAC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAIGGIIGGACIGIIGACCCICIIGICGAAIAIIAIAIIGICGACAGIIGGGGCAACIGG 312
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antibacterial; fungicide; thermostable xylanase activity; dough conditioning; beverage production; nutritional supplement; animal feed; lignin reduction; wood product; xylan; bacterial infection; fungal infection; coccidiosis; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACATATTATTCCGTAAAGGTAAAAATTCAATGAAACACAACACACCAACAGTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u> aargectitatiticgaaaagaaagaagrirgatrecacraaaacrcarcarcaacrigge</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>AACATCTCCATCAACTACAACGCAGCCTTTAACCCGGGGGAATTCCTATTTATGTGTC</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAAGATAGCGGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACATGTCCATAAACTACGGAGCCAACTTCCAACCAAATGGTAATGCGTATTTATGCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              Novel xylanase recombinant polypeptide useful for improving textile texture, treating paper, eliminating microorganisms.
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                                                                                                                                                                                                                                                                                                        Blum
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                                                                                                                                                                                                                                                                                                        Wu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.5%; Score 255; DB 12;
llarity 66.8%; Pred. No. 8.2e-66;
Conservative 0; Mismatches 190;
                                                                                                                                                                                                                                                                                                        Hazlewood G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 185; 570pp; English.
                                                                                                                                                                                                                                                                                                          Callen W, Healey S,
                                                                                                                                                                                                  16-JUN-2003; 2003WO-US019153.
                                                                                                                                                                                                                                  14-JUN-2002; 2002US-0389299P.
                                                                                                                                                                                                                                                                      (DIVE-) DIVERSA CORP.
                                                                                                                                                                                                                                                                                                                                                              2004-099016/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 395; Conserv
                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; ADJ34970
                                                                                                                            WO2003106654-A2.
                                                                                                                                                                                                                                                                                                                         Esteghlalian A;
                                                                                        Unidentified
                                                                                                                                                              24-DEC-2003
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The present sequence represents a RT46B.1 xynB gene and encodes a xylanse enzyme. The present sequence is derived from a gene contained within Dictyoglounus thermophilum strain Rt46B.1 The xylanase is contained within the family of enzymes known as G-Xylanases, and has beta -1,4-xylanase activity. The enzyme has high activity and high thermal stability with optimum activity at 85 degrees Celcius and pH 6.5. The xylanase enzyme is used for the biological bleaching of cellulose products, especially paper pulp. Use of the enzyme ensures that waste streams from the biological bleaching will include less toxic material
                                                         492
                                                                                     567
                                                                                                                 552
                            507
                                                                                                                                             568 AAATGGGAAAGCTTAGGCATGCCAATGGAAAAATGTATGAAACAGCATTAACTGTAGAA 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dictyoglomus thermophilum xylanase gene - used for producing thermally stable enzymes for the bleaching of cellulase products, especially paper
                                                                                   rocadroracorcaadadocacadadocosaacorriricosicadosacarriraaa
TACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATTTAAACAATAT
                           rangaaacecrecenercaarcaecerrerarcarregaeacecracerreaacaarar
                                                         TGGAGTGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGCAACCACTTTAGA
                                                                                                                 GCGTGGGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCGCTTACTGTAGAA
                                                                                                                                                                                                                                                                                                                                                                                          xynB gene; xylanse; enzyme; Dictyoglomus thermophilum strain Rt46B.1;
G-Xylanase; beta -1,4-xylanase activity; activity; thermal stability;
biological bleaching; cellulose product; paper pulp; ss.
                                                                                                                                                                                                                                                                                                                                                                an enzyme with xylanase activity.
                                                                                                                                                                          GGCTATCAAAGTAGCGGAAGTGCTAATGTATATAGCAATACACTAAGAATT
                                                                                                                                                                                            "xylanase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                               AAT90972 standard; DNA; 1190
                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence encoding
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/*tag= b
139. .1146
/*tag= c
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dictyoglomus thermophilum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-503090/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAR-1996;
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                                                 Williams DP,
                                              Groenberg V, Williams DP,
Farrel RL, Bergquist PL,
Herweijer MA, Jones BE;
                                                                                                                                                                                                                                                                                                                                Matches 367; Conservative
                             (KONN ) GIST-BROCADES
                                                                                           WPI; 1996-049690/05.
                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                     P-PSDB; AAR87012
        14-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242
                                                                                                                                               processes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188
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                                                                                                      TAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGGAA 122
                                                                                                                          210 TA---CAGGGAATACAACCATGACTGTATACACAAAGGAAGGTTTAGCTGTCAGTGGAG 266
                                                                                                                                                                                                             Grcariagicacratragaarcaccractraccacarararctraargiaacrccra 380
                                                                                                                                                                                                                                                                                                   GGGTAATTGGCGTCCACCAGGTGCAACCTCTTGGACAGGTTACTATCGACGGTGGTAC
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                                                                                                                                                                                                                                                                              GGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGAAC
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                                                                                                                                                               TITATGCGTCTATGGTTGGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGTTG
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                                                                          CAATGTTAACAACATATTATTCCGTAAAGGTAAAAATTCAATGAAACACACCA
                                                                                                                                                                                                                                                                                                                        ATATGATATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATT
                                                              3 AATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGGAATTTTGGAAAGA
                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xylanase D; xynD gene; thermostable enzyme; paper; pulp; lignin;
delignification; xylan; bleaching; ds.
                                         6
                    Length 1190;
BP; 386 A; 197 C; 277 G; 330 T; 0 U; 0 Other;
                                         Indele
                     DB 2;
                                         0; Mismatches 213;
                    Score 212.2; DB 2
Pred. No. 6.8e-53;
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1. .1107
/*tag= a
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                  32:0%;
ilarity 62.4%;
Conservative
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(revised)
(first ent)
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                               Local Similarity
  Sequence 1190
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25-MAR-2003
12-MAY-1996
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                                Best Local Simi
Matches 369;
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                     Query Match
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AAT08142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treceacteraagatraceractecrecracaatecaarecaariceaarrecrarer 301
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                                                                                                                                                                         Novel xylanase(s) having activity at 80 deg.C. or higher - obtained from anaerobic thermophilic bacteria and used in paper and pulp production
                                                                                                                                                                                                                                                                                                                        A full-length xynD gene (AAT08142) codes for a thermostable G-type xylanase (AAR87012) useful in the pulp and paper industries. The gene wobtd. by genomic walking PCR of DNA from an extremely thermophilic bacterium, strain TG456 (BS 213.94), isolated from a New Zealand hot spring. The gene can be inserted into a vector and used for the produce recombinant xylanase D in microbial host cells, esp. Escherichia coli. (Updated on 25-MAR-2003 to correct DI field.) (Updated on 27-MUG-2003 to correct DI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTAGAGCGTGGGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCGCTTACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 TTAACAATGCACTCTTCAGAACAGGTAAAAAGTTTAGCACTGCATGGAATCAGC-----
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Moody D;
Quax WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1244 BP; 380 A; 215 C; 279 G; 360 T; 0 U; 10 Other;
                            Quax
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  Forster S,
Morgan HW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.1e-50;
2; Mismatches 224;
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     Iverson S,
Daniel RM,
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                                                                                                                                                                                                                                        antibacterial; fungicide; thermostable xylanase activity; dough conditioning; beverage production; nutritional supplement; animal feed; lignin reduction; wood product; xylan; bacterial infection; fungal infection; coccidiosis; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel xylanase recombinant polypeptide useful for improving textile texture, treating paper, eliminating microorganisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.8%; Score 177.8; DB 12; Length 747; 66.1%; Pred. No. 1.1e-42; ive 0; Mismatches 132; Indels 0;
                                                                                                                                                                                                             DNA encoding xylanase from an environmental sample seq id 227.
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Esteghlalian A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 227; 570pp; English.
                                                                                                                ADJ35011 standard; DNA; 747 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                               16-JUN-2003; 2003WO-US019153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JUN-2002; 2002US-0389299P.
                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 26.8
Best Local Similarity 66.1
Matches 257; Conservative
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P-PSDB; ADJ35012.
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609
                               663
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313 CGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGAACATATGATATC 372

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                                                                                                                                                                                          TGGAGTGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGCAACCACTTTAGA 492
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                                                                                    TACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGGATTGCCACATTTAAACAATAT
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Run on:

Sequence:

Searched:

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San Martin)
Av. Gral Paz S/N, INTI, Edificio 24, B 1650 KNA, San Martin, Buenos
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Sequences were basecalled with phred and vector was masked with
crossmatch (see http://genome.washington.edu). Sequences were then
trimmed from both ends to remove low quality bases and masked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trypanosoma cruzi
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
1 (bases 1 to 208)
Aguero,F., Verdun,R., Frasch,A.C.C. and Sanchez,D.O.
A random sequencing approach for the analysis of the trypanosoma
cruzi genome: general structure, large gene and repetitive DNA
families, and gene discovery
Genome Res. 10 (12), 1996-2005 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
                                                                                                                                                                                                                                                                                                                                                                                                                                                              genomic library Trypanosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="epimastigote"
/clone_lib="Trypanosoma cruzi random genomic library"
/note="Vector: pBS(-) (Stratagene); T. cruzi DNA was
randomly sheared using a nebulizer and the 1 to 2 Kb was gel purified and cloned into the dephosphoryated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11116094
On Sep 14, 2000 this sequence version replaced gi:9377651.
Contact: Sanchez D.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              cruzi genomic clone G51N1, genomic survey sequence. AQ908988
                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA
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/organism="Trypanosoma cruzi"
/mol type="genomic DNA"
/strain="CL-Brener"
                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ908988 208 bp DN
GSSTC010294 Trypanosoma cruzi random
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/clone="G51N1"
             AA823781
BF462060
CCN715895
CCN717635
CCN724716
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Class: shotgun.
Location/Qualifiers
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Tel: (54-11) 4580/7255/7
Fax: (54-11) 4752-9639
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 VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
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208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
State University, University Park, PA 16802, USA
Tel: 814 865 9131
Fax: 814 865 9131
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/clone="NotreDame Liverpool-123116"
/clone lib="Notre Dame Liverpool"
/clone lib="Notre Dame Liverpool"
/note="Vector: pECBAC1; Site_1: Hind III; The library was prepared from whole body tissue of newly hatched L1 larvae by David Severson at the University of Notre Dame and
                                                                                                                                                                                                                                                                                                                                                                                           68 AcArcresAccrerrerreAcArrrerGerrerrrrerGereGereGerererer 127
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Aedes aegypti
Eukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
                                                                                                                                                                                                                                                                                                             GTGATGTGTATTGGATTTGTGCTGACACTGACGGCTGTGC
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37.8%; Score 30.6; DB 9; Length 348;
Best Local Similarity 73.6%; Pred. No. 36;
Matches 39; Conservative 0; Mismatches 14; Indels
                                                                                                                                 Length 208;
                                                                                                                                                                                                                     0; Mismatches 24; Indels
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Loftus, B., Shetty,J., Knudson,D. and Severson,D.
end sequencing of Aedes aegypti
Unpublished (2003)
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                                                                                                                                 DB 8;
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Library was provided by David Severson
Seq primer: 17
Class: BAC ends.
                                                                                                                        Score 30.6; 1
Pred. No. 33;
HincII site of the vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Aedes aegypti"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Brendan Loftus
Department of Eukaryotic Genomics
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/strain="Liverpool"
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Tel: 301-838-3543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 CGGCTCATG 79
                                                                                                                                 Query Match
Best Local Similarity
Matches 45; Conserv
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HTC; CAP trapper.
Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .663
                                                                                                                                                                                                                                                                                                                                                                                                                                    e mouse tissues.
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Matches 40; Conserv
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Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 663)
S Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ohno, M., Okazaki, P., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB628216 BIKEN full-length enriched, adult male urinary bladder Musmusculus cDNA clone 9530079L20 5', mRNA sequence.
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length CDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db xref="taxon:44689"
/clone="dds44j03"
/sex="mat A"
/dev stage="Slug stage"
/clone_lib="Dictyostelium discoideum cDNA library, SF"
                                                                                               Distribution and Distribution and Distribution.

Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.

1 (bases 1 to 451)

Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.

Full length conNa of Dictyostellum discoideum at the slug stage bull length conNa of Dictyostellum discoideum at the slug stage Unpublished (2002)

Contact: Tadasu Shin-i

Center For Genetic Resource Information
National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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Mus musculus
                                                                Dictyostelium discoideum
Dictyostelium discoideum
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                   GI:19307918
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                     BJ396832.1
EST.
BJ396832
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wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuurata,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--184-format sequencing pipeline with 184 multicapillary sequencer. Genome Res. 10 (11), 175-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugaharat,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Salto,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AK035636 11533 bp mRNA linear HTC 03-APR-2004 Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530079L20 product:unknown EST, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="RIKEN full-length enriched, adult male urinary bladder"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Journal John Stall, Site 2: BamHI; cDNA library was proper and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [3] primer [3], cDNA was GAGAGAGAAGGATCCAAGAGCTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    395 iraarreierreirikirareiekereiereirrikeereekerekerreiekee 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue_type="urinary bladder"
'dev stage="adult"
'lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="9530079L20"
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Indels
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                                                                                                                                                                                                                                                            DB 3;
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                                                                                                                                                                                                                                                          Score 29.8; DB
Pred. No. 85;
0; Mismatches
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/organism="Bos taurus"
/db_xref="taxon:10090"
/clone="9530079L20"
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/db_xref="taxon:9913"
/clone="ElLU021D12"
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/lab_host="DH108"
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                                                                                                                                                                                                                                                          36.8%;
ilarity 70.2%;
Conservative
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Best Local Similarity
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AV609193
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                                                                                                                         Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes 20499374 °
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adachi, J. Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashida, K., Hayashida, K., Hayashida, K., Hayashida, K., Hayashida, K., Haramoto, K., Hirozane, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koyasa, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsto, N., Santo, H., Sasaki, D., Shibata, K., Shinagawa, A., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tawata, R., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-701-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 330-0045, Japan (E-mail:genome-res@gsc.riken.jp, UKL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,70 full-length cDNAs
Neture 420, 563-573 (2002)
6 (bases 1 to 1533)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the FANTOM Consortium and the RIKEN Genome
                   Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Weth. Enzymol. 303, 19-44 (1999)
99279253
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URL:http://fantom.gsc.riken.jp/
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepare mouse tissues.
                      AUTHORS
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/tissue type="urinary bladder"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AV609193 Sos taurus lung fetus Bos taurus cDNA clone ElLU021D12 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Taksuga, A., Hirotsune, S., Itoh, R., Jitohzono, A., Suzuki, H., Aso, H. and Sugimoto, Y.
Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 GAATTIGAAAAGATTATIGCAGCTITCACAAAGGIATAATGGGITIGICCIGCCAIGCTT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Bos taurus lung fetus"
/note="Vector: pZil; Site_1: Sall; Site_2: Not1; Poly A
was deleted from a Not1 sīte"
                                                                                                                                                                                                                                                                                                                                                                                                                   3 GAATTICAAAAGATIGAGGCIGITIGITITIGIGATGIGITATIGGATTIGIGCIGACACIGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
                                                                                                                                        /note="unknown EST (GB|BE310219, evidence: BLASTN, match=555)"
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Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
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CNSO6ROG 1050 bp DNA linear GSS 05-JUL-2001 T7 end of clone AWOAA016B08 of library AWOAA from strain CLIB 89 of Yarrowia lipolytica, genomic survey sequence.
                                                                                                                                                                                    Gossyptum arboreum

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossyptum.

1 (bases 1 to 804)
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,
Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
Unpublished (2000)
On Jun 8, 2000 this sequence version replaced gi:8379318.

Contact: Wing RA.

Clemson University Genomics Institute
GA Ea0035123f Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_Ba0035123f, mRNA sequence.
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(bases 1 to 1050)
Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J. Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wesset species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db xref="taxon:29729"
/clone="GA_ Ba0035L23f"
/tissue_type="Fibers isolated from bolls harvested 7-10
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Yarrowia lipolytica
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab host="E. coli"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library'
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
1el: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
High quality sequence start: 2
High quality sequence stop: 475.
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/mol_type="mRNA"
/strain="AKA"
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Pred. No. 88;
O; Mismatches
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AL412214.1 GI:12182513
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BE052262.2 GI:13246906
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1 Similarity 73.1%;
38; Conservative C
                                                                                                                                                                 Gossypium arboreum
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Best Local Similarity
Matches 38; Conserv
                                                                ACCESSION
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/mol_type="manna"
/db_xref="taxon:802"
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/clone="tcac0004c.f.24"
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differentiating gonads, gills, interrenal, intestine,
kidney, liver, muscle, ovary, pituitary, testis"
/kidney, liver, muscle, ovary, pituitary, testis"
/lab_nost="from embryos to adults"
/lab_nost="pH108"
/clone_lib="AgeNAE Rainbow trout normalized multi-tissues
library (tcac)"
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I (bases I to 748)
Govoroun, M., Guiguen, Y. and Le Gac, F.
Construction and primary characterization of normalized cDNA Unpublished (2003)
On Jan 14, 2003 this sequence version replaced gi:27746599.
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Campus de beaulieu, RENNES cedex, 35042, France

Tel: 02.23.48.50.09

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Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"
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0; Mismatches 24; Indels
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1. .748
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            GGCTGTGC 70
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CR375533 AGENAE Rainbow trout normalized testis library (tcbi)
Oncorhynchus mykiss cDNA clone tcbi0018c.d.16 5prim, mRNA sequence.
                                                                                                                                                                 Email: szhadotigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Library availability, please contact Pieter de Jong
Library availability, please contact Pieter de Jong
Library availability, please contact Pieter de Jong
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 356 row: N column: 3 Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="RPCI-24"
/clone_lib="RPCI-24"
/note="Vector: pTARBAC1, Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male CS7BL/6J
DNA."
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Oncorhynchus mykiss
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Meopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (Dases 1 to 498)
Govoroun,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization of normalized cDNA
Libraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGAATTTGAAAAGATTGAGGCTGTTGTTTTGTGTATTGGATTTGTGCTGACTG
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                                                                  The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, Fal: 301 838 0208 Fax: 301 838 0208
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Pred. No. 99;
0; Mismatches
                    Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                     1. .706
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="RPCI-24-356N3"
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GSSs: RPCI-24-356N3.TV
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INRA - SCRIBE
Campus de beaulieu, R
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
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Matches 48; Conservative
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                                                                                                                                                                                                                                                                      Direct Submission

Direct Submission

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Direct Submission

Z rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: Sequef@genoscope.cns.fr. Web: www.genoscope.cns.fr.)

This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces survarum, Saccharomyces Saccharomyces harvenii, Aluyveromyces Marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sonbirophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 706)
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note="similar to Saccharomyces cerevisiae ORF YLR068w [
                                                                          Casaregola, S., Neuveglise, C., Lepingle, A., Bon, E., Feynerol, C., Artiquenave, F., Wincker, P. and Gaillardin, C. Genomic exploration of the hemiascomycetous yeasts: 17. Yarrowia lipolytica
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Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
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Pred. No. 92;
0; Mismatches 24; Indels 0,
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1 putative frameshift(s)"
/evidence=not_experimental
                                                                                                                                                                         FEBS Lett. 487 (1), 95-100 (2000)
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/clone="AWOAA016B08"
/clone=lib="AWOAA"
/note="end : T7"
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/strain="CLIB 89"
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Mus musculus
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Best Local Similarity 64.7%;
Matches 44; Conservative
                                                     (bases 1 to 1050)
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/clone_lib="AGENAE Rainbow trout normalized testis library
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BX859701 AGENAE Rainbow trout normalized testis library (tcbi)
Oncorhynchus mykiss cDNA clone tcbi0012d.c.19 5prim, mRNA sequence.
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                                                                                                                                                                                                       479 argaagagagagagacrgaggcrarggccrccccrcriccgrracarrgagrcgaccrig 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGAATTTGAAAAGATTGAGGCTGTTGTTTGTGATGTGTATTGGATTTGTGCTGACTG 60
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                                                                                                                Gaps
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m Y}
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                                                                     Length 623;
                                                                Score 29.2; DB 6; Length 6:
Pred. No. 1.1e+02;
0; Mismatches 28; Indels
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/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
spleen, muscle, and kidney."
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Oncorhynchus mykiss
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/tissue type="testis"
/lab host="DH10B"
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                                                                     36.0%;
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Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
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Best Local Similarity
Matches 46; Conserv
                                                                                                Local Similarity
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BX859701
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Oncorhynchus mykiss
Oncorhynchus mykiss
Bukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 623)
Rexroad, C.E. 3rd, Lee, X.Keele, J.W., Karamycheva, S., Brown, G., Scop, B., Gahr, S.A., Palti, Y. and Quackenbush, J.
Sequence analysis of a rainbow trout cDNA library and creation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA381308 623 bp mRNA linear EST 06-NOV-2002 660794 NCCCWA 1RT Oncorhynchus mykiss cDNA clone 1RT55A08_C_A04 5', CA381308
                                                                     /organism="Oncorhynchus mykiss"
/organism="Oncorhynchus mykiss"
/ol Lype="mRNA" 8022"
/clone="tcbi0018c.d.16"
/tissue type="testis"
/lab_host="DH108"
/clone lib="AGENAE Rainbow trout normalized testis library
(tcbi)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: crexroad@ncccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified by
cross match v0.990329.
Seg primer: AGCGGATAACAATTTCACACAGGA.
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/tissue type="pooled"
/lab_host="DH10B"
/clone llb="NCCCWA IRT"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from brain, gill, liver,
                                                                                                                                                                                                                                                                                                         Resource centre. Francois PIUMI,
Francois Fiumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LEGG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
                                                                                                                                                                                                                                                                                    'note="Vector: pT7T3D-pac; Clone distribution : AGENAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytogenet. Genome Res. 102 (1-4), 347-354 (2003)
Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 725 0351
Pax: 304 725 0351
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Pred. No. 1.1e+02;
0; Mismatches 28; Indels (
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/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxxon:8022"
         row: d column: 16
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Best Local Similarity 62.2%;
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                                 Seg primer: M13R
              Plate: 0018
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Tetrahymena thermophila

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SM Tetrahymena thermophila

SM Tetrahymena. Ciliophora; Oligohymenophorea;

Hymenostomatida; Tetrahymenina; Tetrahymena.

E 1 (bases 1 to 824)

S Gargh, and Pearlman, R.E.

Gargh, dand Pearlman, R.E.

Contact: PEPGb

Department de Biochimie, Universite de Montreal

Email: pepdb-curator@bch.umontreal.ca

Plate: 1388.
                                                                                                                               CNS94115 824 bp mRNA linear EST 05-MAY-2004
TTE00012884 Normalized large Tetrahymena thermophila cDNA, mRNA
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36.0%; Score 29.2; DB 7; Length 824;
Best Local Similarity 62.2%; Pred. No. 1.2e+02;
Matches 46; Conservative 0; Mismatches 28; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Docation/Qualifiers

1. 824
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/db_xref="taxon:5911"
/clone_lib="Normalized large"
368 CCAACCGTGACCGC 381
                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
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Search completed: November 11, 2004, 01:17:01 Job time : 356.127 secs

61 ACGGCTGTGCCGGC 74

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1 ATGAATTTGAAAAGATTGAGGCTGTTGTTTTGTGATGTGTATTTGTGCTGACTG 60

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November 10, 2004, 21:26:43; Search time 423.895 Seconds (without alignments) 8421.106 Million cell updates/sec
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| cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
| cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*
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| cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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11098	119.4 115.2 111.4 110	18.0 17.4 16.8 16.8	1375 1375 942 1002 705	11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	US-10-286-993-1 US-10-307-441-39 US-10-213-990-71 US-10-213-990-70 US-10-213-990-70	Sequence 1, Appli Sequence 39, Appl Sequence 71, Appl Sequence 70, Appl Sequence 68, Appl

Sequence 1, Appli									Sequence 11, Appl	Sequence 12, Appl		Sequence 5, Appli		ednence									-	Seguence 9,	ď	n.	m	ñ	1, A <u>r</u>	m		Sequence 29835, A
US-10-299-393-1	-10-	-10-	3-9	-09-803-4	-10-244-5	US-10-244-596-2	US-10-237-386-10	0-237-	0-244-	0-244-)-244-	10-244-	10-244-		US-10-244-596-9	-10-244	-10-244		-064-60	US-10-244-596-1	US-10-425-115-82922	115-3717	-115-	US-10-237-386-9	US-09-467-368-1	419-969-5	US-10-340-860A-39	3-1	-946-	3-09-149-31	US-10-311-455-793	US-10-369-493-29835
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106	104.8	103.6	96.8	86.8	84.2	84	83.2	83.2	82.6	82.6	82.6	82.6	82.6	82.6	82.6	81	81	79.4	79	77.8	77.2	75.8	73.8	72.4	72.4	54.2	50.4	41		40	38	37.8
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100.0%; Pred. No. 1.5e-183;
tive 0; Mismatches 0;
   4121-40
                                                                                                                                                                                                                    STRAIN: Bacillus
;
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-909-207-1
REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                       LENGTH: 663 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 663; Conservative
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RESULT 2 US-09-909-207-2 ; Sequence 2, Application US/09909207

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TITLE OF INVENTION: Xylanase, microorganisms produced it,

DNA molecule, processes for preparation of this xylanase
and uses thereof
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                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE STREET: 2000 K St., N.W., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Best Local Similarity 100.0%; Pred. No. 1.5e-183;
Matches 663; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/909,207 FILING DATE: 19-Jul-2001 CLASSIFICATION: <Unknown>PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Wilhlem F. Gadiano, Esq. REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/470,953
FILING DATE: 06-JUNE-1995
ATTORNEY/AGENT INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 663 base pairs
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LOCATION: 1..663
                                                                   ERIC DE BUYL
PIERRE LEDOUX
RENE DETROZ
                                             APPLICANT: ANDREE LAHAYE
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STRANDEDNESS: singl
                                                                                                                                                                                                            NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
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general INFORMATION:
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100.0%; Pred. No. 1.6e-183;
iive 0; Mismatches 0;
                                                                                                                                                                                                                      STRAIN: Bacillus
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-909-207-4
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; Sequence 5, Application US/09909207
; Patent No. US20020115181A1
; GENERAL INFORMATION:
; APPLICANT: ANDREE LAHAYE
                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
              INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 663; Conservative
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AACCACTITAGAGCGIGGGAAAACTIAGGGAIGAATAIGGGGAAAAIGIATGAAGICGCG 540
                                                                          241 TATTTATGCGTCTATGGTTGGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGT
                                                                                                                                                                      301 TGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.25
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ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION UNMERS: US/09/909,207
FILING DATE: 19-Jul-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/470,953
FILING DATE: 06-JUNE-1995
ATTORNEX/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09909207 Patent No. US20020115181A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ANDREE LAHAYE
ERIC DE BUYL
PIERRE LEDOUX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA
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ERIC DE BUYL
PIERRE LEDOUX
RENE DETROZ
TITLE OF INVENTION: Xylanase, microorganisms produced it,
DNA molecule, processes for preparation of this xylanase and uses thereof
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                                                                                                                                                                                                                                                                                                                                        540
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481 AACCACTTTAGAGCGTGGGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCG
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                                        241 TAITTATGCGICTATGGTTGGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGT
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CORRESPONDENCE ADDRESSE:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Sulte 200
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version #1.25
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COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
APPLICATION NUMBER: US/09/909,207
FILING DATE: 19-UN1-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/470,953
FILING DATE: 06-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 20-429-0625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/09909207
Patent No. US20020115181A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ANDREE LAHAYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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US-09-909-207-10
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                                              Aramase, microorganisms produced it,
DNA molecule, processes for preparation of this xylanase
and uses thereof
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                                                                                                                                                                                                                           COMPURY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                       & LIONE
       ERIC DE BUYL
PIERRE LEDOUX
RENE DETROZ
OF INVENTION: Xylanase, microorganisms.
                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON
STREET: 2000 K St., N.W., Suite 200
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/909,207
FLING DATE: 19-Jul-2001
CLASSIFICATION: «Unknown»
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/470,953
FILING DATE: 06-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: sig_peptide
LOCATION: 1..81
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 202-429-0625
TELEPAX: (202) 239-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: mat_peptide
LOCATION: 82..744
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                      SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1..744
                                                                                                                                                                                            CITY: Washington STATE: D.C.
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NAME/KEY:
                                                                                                                    NUMBER OF
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                                                                  TITLE
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Best Local S:
Matches 663,
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TITLE OF INVENTION: Xylanase, microorganisms produced it,

DNA molecule, processes for preparation of this xylanase
and uses thereof
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                                                                                                                                                                                                                                                                         COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/909,207
FILING DATE: 19-Jul.-2001
CLASSIFCATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
ATORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 08/470,953
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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100.0%; Pred. No. 2.2e-183;
ive 0; Mismatches 0;
                                                                                                                                    GILSON 2
                                                                                                 NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSES: WILLIAN BRINKS HOFER
STREET: 2000 K St., N.W., Suite
CITY: Weathington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 620..700
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-909-207-11
                                                                                                                                                                                                                         ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1513 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: mat_peptide
LOCATION: 701..1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 620..1363
                               RENE DETROZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.'
Matches 663; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN: Bacillus
                PIERRE
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                                                                                                                                                                                                                                                   Length 1513;
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                                                                                                                                                                           STRAIN: Bacillus
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1513 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Patent No. US20020115181A1
GENERAL INFORMATION:
                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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APPLICANT: Mantyla, Arja
APPLICANT: Paloheimo, Marja
APPLICANT: Labretto, Raija
APPLICANT: Fagerstrom, Richard
APPLICANT: Suominen, Tarja
APPLICANT: Suominen, Pirkko
APPLICANT: Suominen, Pirkko
APPLICANT: WENNINON: Production and Secretion of Proteins in Filamentous
TITLE OF INVENTION: Fungi
FILE REPRENCE: 1716.0344004
CURRENT APPLICATION NUMBER: US/10/286,993
CURRENT FILING DATE: 2002-08-13
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0; Mismatches 176;
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REFERENCE DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
TELEFAX: 202-371-2540
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                                                                                 UMBER: US 08/282,001
29-JUL-1994
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Publication No. US20030148453A1
GENERAL INFORMATION:
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MOLECULE TYPE: DNA (genomic)
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Matches 238; Conservative
        PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 29-JUL-1
CLASSIFICATION:
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LOCATION:
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APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarija
TITLE OF INVENTION: Production and Secretion of Proteins of NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
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| Sequence 39, Application US/103016436A1
| Publication No. US2030166236A1
| GENERAL INFORMATION:
| APPLICANT: SUNG, Wing L.
| APPLICANT: SUNG, Wing L.
| APPLICANT: Mational Research Council of Canada TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity TITLE OF INVENTION: MOMBER: US/10/307,441
| CURRENT APPLICATION NUMBER: US/10/307,441
| CURRENT APPLICATION NUMBER: US/10/307,441
| PRIOR PILING DATE: 2001-05-31
| PRIOR FILING DATE: 2001-05-31
| PRIOR FILING DATE: 2000-05-31
| WUMBER OF SEQ ID NOS: 51
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NOS: 51
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Pred. No. 3.8e-24;
0; Mismatches 176; Indels
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       PRIOR APPLICATION NUMBER: US/09/120,804
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1997-01-24
PRIOR PILING DATE: 1997-01-26
PRIOR APPLICATION NUMBER: US 08/590,563
PRIOR APPLICATION NUMBER: US 08/590,563
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LUCATION: (303)..(1337)
; OTHER INFORMATION: Product= AM35 xylanase US-10-286-993-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 57.1%;
Matches 238; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
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APPLICANT: Jang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Storms, Res
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
TITLE OF INVENTION: NUCLEIC ACIDS OF USE
FILE REPERENCE: 10182-019-99
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT APPLICATION NUMBER: US/10/213,990
SURRENT FILING BATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOPTWARE: FRASESQ for Windows Version 4.0
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                                                                                                DB 15; Length 596;
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OTHER INFORMATION: Description of Artificial Sequence: TrX
                                                                                             Query Match
17.4%; Score 115.2; DB 15; Length
Best Local Similarity 57.7%; Pred. No. 4.3e-23;
Matches 226; Conservative 0; Mismatches 163; Indels
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; Sequence 71, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
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US-10-213-990-71
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                        US-10-307-441-39
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LENGTH: 942
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APPLICANT: Jang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Bussey, Howard
APPLICANT: Bussey, Howard
APPLICANT: Roemer, Terry
TITLE OF INVENTION: BUZYMES AND METHODS OF USE
FILE REPERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT PILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 ceresecaacrireresersaaaasese-----resaacceresaaseseraserace 293
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Pred. No. 3.5e-21;
0; Mismatches 267;
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                                                                                                                                                                                                             ; Sequence 68, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
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Query Match
Best Local Similarity 51.9°
Matches 298; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ... (705)
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; LOCATION: (1).
US-10-213-990-68
                                                                                                                                                RESULT 12
US-10-213-990-68
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LENGTH: 705
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Publication No. US20030082595A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jiang, Howard
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Roomer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
FILE REFERENCE: 10182-019-999
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                                                                                          CATTTAAACAATATTGGAGTGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCA 478
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                                       GGGGCA----ACTGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        539 CGCTTACTGTAGAGGCTATCAAAGTAGCGGAA 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         558 TCAAAGTAGCGGAA 571
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Matches 216; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Aspergillus
US-10-213-990-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-10-213-990-70
                                                                                                                                                                                    359
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546 TGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAATGT
        Sequence 64, Application US/10213990
Publication No. US20030082595A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              15.8%;
55.8%;
                                                                                                                                                                                                                                                                                                                                                                               221; Conservative
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US-10-213-990-64
                                                                                                                                                                                                                                                                                                                                                            Similarity
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US-10-213-990-65
JS-10-213-990-64
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Best Local S
Matches 221
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                                                                           APPLICANT: Fish, Neville Marshall
APPLICANT: Fish, Neville Marshall
APPLICANT: Haigh, Nigel Paterson
TITLE OF INVENTION: PENICILIINE FUNICULOSUM STRAIN USEFUL
TITLE OF INVENTION: FOR THE PRODUCTION OF ENZYMES
FILE REFERENCE: A32917-PCT-USA-I (072667.0183)
CURRENT APPLICATION NUMBER: US/10/299,393
CURRENT APPLICATION NUMBER: 09/462,246
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: 1998-05-06
NUMBER OF SEQ ID NOS: 14
SEQ ID NO: 2899 ID NOS: 14
LENGTH: 2898
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Pred. No. 4.5e-20;
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               Sequence 1, Application US/10299393
Publication No. US20030108642A1
GENERAL INFORMATION:
APPLICANT: Sabatier, Alain
                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Penicillium funiculosum
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ilarity 56.5%;
Conservative
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LOCATION: (724)...(730)
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LOCATION: (570)...(576)
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218; Conserv
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      -10-299-393-1
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Sequence 65, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; TITLE OF INVENTION: NUCLEIC ACIDS OF USE
FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
APPLICANT: Jiang, Bo.
APPLICANT: Bussey, Howard
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 64
LENGTH: 712
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Pred. No. 5.2e-20;
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; LENGTH: 666 ; TYPE: DNA ; ORGANISM: Aspergillus ; FATURE: ; NAME/KEY: CDS ; LOCATION: (1)...(666) US-10-213-990-65

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263 CTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGTTGGGGCAACTGGCGTCCACCA- 321
                                                                                                                                                          392 CGGGAGCCACCCATCTCGGCACCGTCGAGAGCGACGGGGCCACGTACAACCTCTACAAGA 451
                                                                                                                                                                                                                                                                      380 CTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGTG 439
                                                                                                                                                                                                                                                                                             440 TICGAAGAICGAAACGCACGAGIGGCACGAITICIGICAGCAACCACTIIAGAGCGIGGG 499
                                                                                                                                                                                                                                                                                                                                                                                                          500 AAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCGCTTACTGTAGAAGGCTATC 559
                                                                                                                                                                                                                                                                                                                                                                          572 GAAATGCGGGTCTGCAATTGGGGAACTTTGACTATATGATTGTTGCGACGGAGGGGTACC 631
                                                                    203 TAAACTACGGAGCCAACTTCCAACCAAATGGTAATGCGTATTTATGCGTCTATGGTTGGA
Query Match 15.6%; Score 103.6; DB 14; Length 666; Best Local Similarity 56.3%; Pred. No. 1.1e-19; Matches 215; Conservative 0; Mismatches 164; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             560 AAAGTAGCGGAAGTGCTAATGT 581
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CR133022 0X1_9_D10
CF867983 tricol3xe
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CD458837 Fg08 04b1
AQ160513 mgxb00065
AQ447125 mgxb00031
AQ35248 mgxb00031
AQ35248 mgxb0001B
AQ180559 mgxb0001B
AQ39120 mgxb0001B
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Sun, F., Sullivan, R., Lim, S., Eastman, A. and Pratt, L.H.

Sun, F., Sullivan, R., Lim, S., Eastman, A. and Pratt, L.H.

Unpublished (2003)

Other ESTs: Oxl 9 D10.91 A002

Contact: Cordonnier-Pratt MM

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Pax: 706 583 0210
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Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science, plant material and RNA prepared at Texas A & M University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
'University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
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ramet clones until predawn needle water potential reached -1.75 MPa. On day 7 roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into p5L1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Sorghum.
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Pred. No. 4.8e-17;
0; Mismatches 144; Indels
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CN135U22
OX1 9 D10.G1 A002 Oxidatively-stressed leaves and roots Sorghum bicolor cDNA clone OX1 9 D10 A002 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 GGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGTTGGGGGCA---ACTGGCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATTTAAACAATATTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 AGACCACCGCTACAACCAGCCCTCTATCGACGGCCAACAGACCTTCAACCAGTACTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  437 GTGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGCAACCACTTTAGAGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCATAAACTACGGAGCCAACTTCCAACCAAATGGTAATGCGTATTTATGCGTCTATGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 ccarcaacrardeceerrerfricaeceercaeeeraaceeeraecrordeereraeeeer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         317 CACCAGGAGCAACGCCTAAGGGGGACCATCACTGTTGATGGAGGAACATATGATATCTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     341 CCATCCGCCGCACAACAGCGCAGCGGCGCCGTCAACATGCTGCAGACTATCTTCAATGCTT
                                                                                                                                                                                                                                                                                                                                                                            Length 728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              557 ATCAAAGTAGCGGAAGTGCTAATGTATATAGCAATAC 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             accadadecadredarctretretraterateredade 497
                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 180;
                                                                                                                                                                                                                                                                                                                                                                        Score 93; DB 7;
Pred. No. 2e-15;
organism="Sorghum bicolor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sorghum bicolor (sorghum)
Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CN133022.1 GI:45963542
                                                                                                                                                                                                                                                                                                                                                                        14.0%;
                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 53.9
Matches 214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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CF867983 1-OCT-2003 tricol3xe09.bl T.reesei mycelial culture, Version 6 October 2003 Hypocrea jecorina cDNA clone tricol3xe09, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotta; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

1 (Bases I to 74a)

1 (Bases I to 74a)

1 (Bases I to 74a)

1 (Bases I to 74a)

Teunissen, P.J.M., van Solingen, P., Dankmeyer, L., Mitchell, T.K., Ward, M. and Dean, R.A.

Characterization of the protein processing and secretion pathways in a comprehensive set of expressed sequence tags from Trichoderma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACATGTCCATAAACTACGGAGCCAACTTCCAACCAAATGGTAATGCGTATTTATGCGTC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              413 TACGGCTGGTCCCGCAACCCCCTGATCGACTACATCGTCGAGAACTTTGGCACCTAC 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313 CGTCCACCA---GGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGAACATATGAT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      473 AACCCGTCCACGGGCGCCACCAAGCTGGGCGAGGTCACCTCCGACGGCAGCGTCTACGAC 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGGATTGCCACATTTAAACAA 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATTGGAGTGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGCAACCACTTT 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAGCGTGGGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCGCTTACTGTA 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="mycelia"
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2003"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pREP1Y; Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          533 ATTTACCGCACGCAGCGCCTCAACCAGCCGTCCATCATCGGCACCGCCACCTTTTACCAG
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55.0%; Pred. No. 4.5e-15;
tive 0; Mismatches 162; Indels
                                                                                                                                                                                                Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEMS Microbiol. Lett. 230 (2), 275-282 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db xref="taxon:51453"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="tric013xe09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ralph dean@ncsu.edu
Seg primer: LT-F1 primer.
Location/Qualifiers
                                                                                                                                                          CF867983.1. GI:38122635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 919-513-0020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 919-513-0024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGGCT 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 202; Conser
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                                                                                                                                                               VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                    DEFINITION
                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                   CF867983
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                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Collivar="BTK623"
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/db Arsef="Laxon:4558"
/db Arsef="Laxon:4558"
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/clone=loX1 9 D10 A002"
/clone=loX3 = D10 A002"
/clone=loY3 = Laxon:4558"
/clone=loY3 = Laxon: The phage-resistant E. coli"
/clone=loY3 = Laxon: The library was prepared from poly4+
RNA from oxidatively stressed, hydroponically grown
sorghum seedlings. At 8 days of age, growth medium was
supplemented with hydrogen peroxide to 0.003* and leaves
were misted with 10 um methyl viologen. Leaves and roots
were harvested at 3, 12 and 27 hr after treatment and all
tissue pooled. Double-stranded cDNA was cloned
unidirectionally into different Draili sites of the
phases-Fi3 vector. (5-prime Draili site is CACCATGTG). XhoI excises the cDNA
                                                                                                                                                                                      Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Pired quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGTTGGGGCA---ACTGGCGTC 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Other ESTs: OX1 9 D10.bl A002
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 543 1860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
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Pred. No. 2e-15;
0; Mismatches 180; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           Seq_primer: Sugs (CTTCTGCTCTAAAAGCTGCG)
Location/Qualifiers
1. .772
/organism="Sorghum bicolor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.0%;
ilarity 53.9%;
Conservative
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Best Local (
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Matches
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                    COMMENT
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/organism="Sorghum bicolor"
/wol type="mRNA"
/wol type="mRNA"
/wol type="mRNA"
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/db xref="traxon:4558"
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/lab host="bihlo-T1 phage-resistant E. coli"
/dlone lib="Ethylene-treated seedlings"
/dlone lib="Ethylene-treated seedlings"
/dlone lib="Ethylene-tranged from polyth-RNA from seedlings grown in hydroponic culture. At 8 days of age, medium was supplemented with 0.5 mM 1-aminocyclopropane-1-carboxylic acid (ACC) to induce endogenous ethylene (FTH) production. Roots and shoots were harvested after 27 and 72 hr and material from both time points was combined prior to RNA isolation. Double-stranded cDNA was cloned unidirectionally into different Drall sites of the pwBl85-FL3 vector (5-prime Drall site is CACTGTGTG, 3-prime Drall site is CACTGTGTG). Xhol excises the CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryoum Living Tracheophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

(bae; Panicoideae; Andropogoneae; Sorghum.

(cordonnier-Pratt, M.-M., Wentzel, V., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Shah, M., Salzman, R., Chua Tan, N., Gonzalez, M., Lane, S., Miller, V., Nanda, P., Olaseinde, O., Eastman, A. and Pratt, L.H.

An EST database from Sorghum: 1-aminocyclopropane-1-carboxylic acid
                                                                                                                                                                                                 T38 bp mRNA linear EST 04-JUN-2003 ETH1_48 B06.gl_A002 Ethylene-treated seedlings Sorghum bicolor CDNA COLONE ETH1_48_B06_A002 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCATAAACTACGGAGCCAACTTCCAACCAAATGGTAATGCGTATTTATGCGTCTATGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 738;
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53.5%; Pred. No. 1.4e-13;
tive 0; Mismatches 174; Indels
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2003)
Other ESTs: ETH1 48 B06.bl A002
Contact: Cordonnier-Pratt MM
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Sorghum bicolor
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Fax: 706 583 0210
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                                                                          768 GGAGGGT 774
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                        ઠે
                                                                                                                                      CB898036 tricol3xe09 T.reesei mycelial culture, Version 3 april Hypocrea jecorina cDNA clone tricol3xe09, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               528 AACCCGTCCACGGCCCCACCAAGCTGGGCGAGGTCACCTCCGACGCCAGCGTCTACGAC 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370 ATCTACGAGACTCTTAGAGTCAATCAACCTCCATTAAGGGGATTGCCACATTTAAACAA 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   588 ATTIÁCCGCACGCAGCGCGTCAACCAGCCGTCCATCACCACCACCCTTTTACCAG 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          708 Arcicchigacorchacaadaccricacaricadaadariaaninaccaanininaccaia 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 AACATGTCCATAAACTACGGAGCCAACTTCCAACCAAATGGTAATGCGTATTTATGCGTC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253 TATGGTTGGACTGTTGACCCTCTTGTCGAATATTATTGTTCGACAGTTGGGGGCAACTGG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAGCGTGGGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCGCTTACTGTA 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db.cxef="tracon:51453" /db.cxef="tracon:51453" /clone="tricol3xe09" /dev stage="mycelia" /clone lib="Treesei mycelia" culture, Version 3 april" /note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           408 AACAAGGTCATCAACTTCTCGGGCAGCTACAACCCCAACGGCAACAGCTACCTCCGTG
                                                                                                                                                                                                                                                                                                                                                                                                         Hypocreomycetidae; Hypocreales; Hypocreace; Hypocrea.

1. (bases 1 to 799)
1. (bases 1 to 799)
1. (bases 1 to 799)
2. (bases 1 to 799)
3. (bases 1 to 799)
4. (bases 1 to 799)
5. (bases 1 to 799)
5. (bases 1, Brown, D.E., Dankmeyer, L., Fouek, T.D., England, G.J., Kelley, A.S., Meerman, H.J., Mitchell, T. Mitchinson, C., Ollvares, H.A., Teunissen, P.J., Yao, J. and Ward, M.
Transcriptional regulation of biomass-degrading enzymes in the filamentous fungus Trichoderma reessi
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                                                                                                                                                                                                                                                                                                                        Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             925 Page Mill Road, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. 278 (34), 31988-31997 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: (550) 846-7635
Fax: (650) 621-7817
Email: Pforeman@genencor.com
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Location/Qualifiers
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                                                                                                                                                                                                                                                                      CB898036.1 GI:30112694
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713 GGAGGGT 719
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/tissue_wype="Protoplasts"
/lab_hogt="B. coli DH10B"
/clone lib="Cudi Rice Blast BAC Library"
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devestating fungal diseases
of rice world wide. It is a filamentous ascomycete with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ160513 603 bp DNA linear GSS 09-SEP-1998 mgxb0006C21r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
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                                                                                                                                                                                                                                                      GGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGTTGGGGCAACTGGCGTCCAC 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         663 GGAGATCTGCTGGCATGAACCTCGGAAACCACTACTACCAGATTCTGGCCACTGAGGGTT 722
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Y.Y., Zhul.H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M. Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                        320 CAGGA---GCAACGCCTAAGGGGACCATCACTGTTGATGGAGGAACATATGATATCTACG
                                                                                                                                                                                                                                                                                                                       gakcccccccccrcdrcdarkcrkccrcarcdachrracdcrrcrracaacccc
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Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
                                                                                                           CCATAAACTACGGAGCCAACTTCCAACCAAATGGTAATGCGTATTTATGCGTCTATGGTT
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100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seg primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 424.
                                          Indele
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0; Mismatches 186;
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Clemson University Genomics Institute
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/organism="Magnaporthe of /mol_type="genomic DNA" /strain="70-15"
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           52.4%;
       Best Local Similarity 52.49
Matches 208; Conservative
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Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
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Watson, N.J., Heyer, Chapados, J., Couroux, P., Harris, L.J.,
Hattori, J., Lacroix, C., Ouellet, T., Robert, L.S., Singh, J.A.,
Sprot, D. and Tinker, N.A.
A CDNA library prepared from Fusarium graminearum grown on a Complex plant substrate
Unpublished (2003)
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Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
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/clone="Fg08 04b10"
/tissue_type="mycelium"
/dev stage="Asexual"
/lab_nost="E. coli DH10B"
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Email: watsonrj@agr.gc.ca
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a haploid genome (n=7) of approximately 40 Mpp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25% genome coverage. High density colony filters are available upon request."
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Y. X., Zhi,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,

Phillips, K., Sasinowski,M. Wing,R.A. and Dean,R.A.

A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes
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12.5%; Score 82.8; DB 8; Length 603;
Best Local Similarity 52.8%; Pred. No. 1.6e-12;
Matches 227; Conservative 0; Mismatches 197; Indels
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Fax: 864 656 4293
Eaxi: 864 656 4293
Seq primer: TAATACGACTCACTATAGGG
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Clemson University Genomics Institute
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KEYWORDS
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| ....o', cognism="Magnaporthe grisea" | ...o', cognism="Magnaporthe grisea" | /mol_type="genomic DNA" | /mol_type="genomic DNA" | /mol_type="genomic DNA" | /mol_type="location of the content of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the cost of the
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetes incertae sedis, Magnaporthaceae, Magnaporthe.
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Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
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54.6%; Pred. No. 2.5e-12;
tive 0; Mismatches 168;
                                                                                   263.
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Class: BAC ends
High quality sequence stop: 2
Location/Qualifiers
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/lab host="s. coli DH108"
/lab host="s. coli DH108"
/loce=11b="CUGIR1ce Blast BAC Library"
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/note="Vector: pBACWICH; Site_1: High assenses
/note="Vector: pBACWICH; Site_1: High density represents greater
than 25x genome coverage. High density colony filters
are available upon request."
                               AQ160254 1750 bp DNA linear GSS 09-SEP-1998 mgxb0003L19r CUGI Rice Blast BAC Libbary Magnaporthe grisea genomic
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                                                                                                                                                                                                                                    (bases 1 to 750)
Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
Phillips,K., Sasinowski,M. Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
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Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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                                                                                                                                                                                                                                                                                                                                                         Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
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                                                                      cione mgxb0003L19r, genomic survey sequence.
AQ160254
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llarity 54.1%; Pred. No. 2.5e-12;
Conservative 0; Mismatches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        grisea"
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Location/Qualifiers
1. 750
/organism="Magnaporthe g/mol_type="genomic DNA" /strain="70-15"
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/clone="mgxb0003L19r"
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Seg primer: GGAAACAGCTATGACCATG
Class: BAC ends
                                                                                                                  GI:3557243
                                                                                                                                                                                                                                                                                                                                        Unpublished (1998)
                                                                                                                AQ160254.1
GSS.
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Matches 236; Conserv
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                                                                                                   Clemson University
100 Jordan Hall, Clemson Universiy, Clemson,
Tel: 864 656 5737
Exa: 864 656 4293
Email: rdean@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 12.4%; Score 82.2; DB 8; Best Local Similarity 54.1%; Pred. No. 2.5e-12; Matches 236; Conservative 0; Mismatches 189;
                                                                  Contact: Dean RA
Clemson University Genomics Institute
                                                                                                                                                                                                   Seg primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 321.
Location/Qualifiers
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445 TACTCGGGCAGCTACAGCCCCCAGGGCAACTCATACCTGGCCGTCTACGGCTGGACGCGC 268 GACCCTCTTGTCGAATATTATATTGTCGACAGTTGGGGCAACTGGCGTCCACCA---GGA

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210 CGCTACAACCAGCCCTCCATCGACGGCACCAAGACCTTTCAGCAGTTCTGGTCGGTGCGC 151
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W.Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
Phillips,K., Sasinowski,M. Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
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                                                                   445 AGATCGAAACGCACGAGGGCACGATTTCTGTCAGCAACCACTTTAGAGCGTGGGAAAAC
                                                                                                                                           150 CGCAACAAGGGGCCAGCGGCACCGTCACCTTTGCCAACCACGTCAACGCTGGCGCAAC
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Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
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Magnaporthe grisea
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clone="mgxb0021M08r"
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strain="70-15"
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High quality sequence start: 49
High quality sequence stop: 468.
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583 bp DNA linear GSS 06-MAR-1999 mgxb0001B24f CUGI Rice Blast BAC Library Magnaporthe grisea genomic AQ399120 AQ399120 AQ399120.1 GI:4370147
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1 (V. Z. Mil, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Sasinowski, M. Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
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Magnaporthe grisea
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetes incertae sedis, Magnaporthaceae, Magnaporthe.
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Clemson University Genomics Institute
Clemson University
Cloud Outdan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
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Seg primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 411.
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/strain="70-15"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1998)
RESULT 13
AQ399120/c
                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
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AUTHORS
                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
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                                                                                                           LOCUS
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Gaps

Indels 11;

Length 786;

12.3%; Score 81.6; DB 8; I llarity 54.1%; Pred. No. 3.8e-12; Conservative 0; Mismatches 189;

Similarity

Query Match Best Local S: Matches 236,

236;

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numerous aspects of the fungal pathogen for studying numerous aspects of the fungal-host interaction. In corder to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25% genome coverage. High density colony filters are available upon request."
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                                                                                                                                                                                                                                                                                                                                            154 AAAAAATTCAATGAAACACAAACACACCAACAAGTTGGTAACATGTCCATAAACTACGGA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTGTCGAATATTATATTGTCGACAGTTGGGGCAACTGGCGTCCACCA---GGAGCAACG 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  391 AATCAACCCTCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGTGTTCGAAGATCG 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACCAGCCCTCCATCGACGCACCAAGACCTTTCAGCAGTTCTGGTCGGTGCGCCCCCAAC 146
                                                                                                                                                                                                                                                                                                                                                                                      AAGAAAAAAGAGAGACTAACATCAACAACAACAAAAAAGGCGGCGTCATCAACTACTCG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCAACTTCCAAATGGTAATGCGTATTAATGCGTCTATGGTTGGACTGTTGACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCAGCTACAGCCCACACGCCAACTCATACCTGGCCGTCTACGGCTGGACGCCAACCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331 CCTAAGGGGACCATCACTGTTGATGGAGGAACATATGATATCTACGAGACTCTTAGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACCGCGGGGTCCTTCACCTCGGACGCCCTACGACATCCTGGTCAGCACCCGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 AAGCGCCCAGCGGCACCGTCACCTTTGCCAACCACGTCAACGCCTGGCGCAACGCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAACGCACGAGGCACGATTTCTGTCAGCAACCACTTTAGAGCGTGGGAAAACTTAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes
Sordariomycetes incertae sedis, Magnaporthaceae, Magnaporthe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome

(Unpublished (1998))

COntact: Dean RA

Clemson University

Clemson University

100 Jordan Hall, Clemson Universiy, Clemson, SC 29634

Tel: 864 656 5737

Fax: 864 656 4293

Email: rdean@clemson.edu
Seg primer: TAATAGGACTCACTATAGGG
                                                                                                                                                                                                                                                                                               3,
                                                                                                                                                                                                                                     12.3%; Score 81.4; DB 8; Length 583; 52.8%; Pred. No. 4.1e-12;
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Magnaporthe grisea (anamorph: Pyricularia grisea)
                                                                                                                                                                                                                                                                                            0; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence start: 50 High quality sequence stop: 443. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             511 ATGAATATGGGGAAAATGT 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          crcaaccrceccaacres 67
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                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 200; Conserv
                                                                                                                                                                                                                                                                                                                                                                                             445
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                                                                                                                                                                                                                                                  Query Match
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AQ396475/c
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AUTHORS
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/kissue_type="Protoplasts"
//lab host="E. coli DH108"
//lab host="E. coli DH108"
//lab host="E. coli DH108"
//clone_lib="CUGI Rice Blast BAC Library"
//clone_lib="CUGI Rice Blast BAC Library"
//note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
//note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
//note="Vector: pBACWICH; Site_1: HindIII; Site_blast is one of the most devestating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (wide ingal pathogen for studying
numerous aspects of the fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25x genome coverage. High density colony filters
are available upon request."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   318 regregesecedecaaceseeseserreaceregaaceaceaceracaacarecre 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              436 AGTGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGCAACCACTTTAGAGCG 495
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Keon, J.P. R., Hargreaves, J.A., Antoniw, J.F. and Hammond-Kosack, K.
Analysis of expressed sequence tags from the wheat fungal leaf
blotch pathogen, Mycosphaerella graminicola (anamorph Septoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 TTATTCCGTAAAGGTAAAAATTCAATGAAACACAAAACACACCAACAAGTTGGTAACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        376 GAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATTTAAACAATATTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 TCCATAAACTACGGAGCCAACTTCCAACCAAATGGTAATGCGTATTTATGCGTCTATGGT
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Chaetothyriomycetes incertae sedis; Mycosphaerellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 76.6; DB 8; Length 5
Pred. No. 9.6e-11;
0; Mismatches 170; Indels
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Fungal Genet. Biol. (2004) In press
/db_xref="taxon:148305"
/clone="mgxb0010M14f"
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Mycosphaerella graminicola
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AJG38869.1 GI:47031926
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Best Local Similarity 53.7%;
Matches 204; Conservative
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Best Local Similarity 55.6%; Pred. No. 1.1e-10;
Matches 168; Conservative 0; Mismatches 131; Indels
Contact: Keon J
Plant Pathogen Interactions Division,
Plant Pathogen Interactions Division,
Rothamsted Research,
Harpenden, Herts, UNITED KINGDOM
Tel: +44 (0)1582 763133
Tex: +44 (0)1582 760981
Email: john. Keon@bbsrc.ac.uk
Insert Length: 800 Std Error: 100.00
Seq primer: M3 reverse.

1. :617
Cocation/Qualifiers

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Scoring table:

Searched:

Minimum DB Maximum DB

Database

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unclassified.

1 (bases 1 to 744)

De, B.E., Lahaye, A., Ledoux, P. and Detroz, R.

Xylanase, microorganisms for its production, DNA molecules, process
of preparation and use thereof

Patent: EP 0698667-A 4 28-FEB-1996;
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Best Local Similarity 100.0%; Pred. No. 1.9e-187;
Matches 744; Conservative 0; Mismatches 0;
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AUTHORS
TITLE
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A48231 Sequence 11
AR13055 Sequence 11
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Copyright (c) 1993 - 2004
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(S De, B.E., Lahaye, A., Ledoux, P. and Detroz, R.

Xylanase, Microcraganisms for its production, DNA molecules, process of preparation and use thereof.

LOSTONIAN (BE)

SOLVAY (BE)

Other publication BE 1008751 960702

Other publication BE 8092284 960305

Other publication PI 953578 960127

Other publication PI 953578 960127

Other publication AP 2508695 960208.

Other publication AP 2508695 960208.

Other publication AP 2508695 960208.

In 744

//Organism="unidentified"
//mol_type="unassigned DNA"
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De Buyl,E., Lahaye,A., Ledoux,P. and Detroz,R.
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1 (bassisted.)

B BUYL, B., Lahaye, A., Ledoux, P. and Detroz, R.

Xylanase, microorganisms producing it, DNA molecules, methods preparing this xylanase and uses of the latter

Patent: US 6346407-A 4 12-FEB-2002;
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/wol_type="unassigned DNA"
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Db 1040 ACCATCACTGTTGATGGAGGAACATATGATATCTACGAGACTCTTAGAGTCAATCAA	Db 1160 AGTGGCACGATTCTGTCACCACTTTAGAGCGTGGGAAAACTTAGGGATGATATG 1219	RESULT 6 A48232 LOCUS LOCUS LOCUS DEFINITION Sequence 11 from Patent BP0698667. ACCESSION A48232 VERSION VERSION KEYWORDS SOURCE ORGANISM unidentified ORGANISM (1 bases 1 ted) NCLASSIFIED REFERENCE 1 (bases 1 ted) NCLASSIFIED REFERENCE 1 (bases 1 ted) AUTHORS De, B. B., Lahaye, A., Ledoux, P. and Detroz, R. TITLE Xylanase, microorganisms for its production, DNA molecules, process	JOURNAL Patent: EP 0698667-A 11 28-FEB-1996; SOLVAX (RE) COMMENT Other publication BE 1008751 960702 Other publication BE 9608570 960604 Other publication BR 9603454 960305 Other publication JP 8092284 960409 Other publication GA 2154628 960127 Other publication CA 2154628 960127 Other publication AU 2508695 960208. FEATURES 1 . 1513 FOURTH PROGRAMMENT OF THE PROGRAMMENT	CDS (db_xref="taxon:32644" CDS (50.:1366 Anote="unnamed protein product" (codon start=1	ORIGIN Query Match Query Match Best Local Similarity 100.0%; Score 744; DB 6; Length 1513; Best Local Similarity 100.0%; Pred. No. 1.8e-187; Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 ATGAGACAAAGAAATTGAGTTTTAGCTTTTTTTTTTTTT
Qy 661 GTATATAGCAATACACTAAGAATTAACGGTAACCTCTCTCAACTATTAGTAATGACGGG 720 Db 661 GTATATAGCAATACACTAAGAATTAACGGTAACCCTCTCTCAACTATTAGTAATGACGAG 720 Qy 721 AGCATAACTTTGGATAAAAACAAT 744 Db 721 AGCATAACTTTGGATAAAACAAT 744	A48231 LOCUS DEFINITION Sequence 10 from Patent EP0698667. DEFINITION A48231 A48231 A48231 A48231 A48231 A48231 A48231 A48231 GI:2302078 CETWORDS SOURCE Unidentified Unclassified. REFERENCE AUTHORS TITLE Xylangse, microorganisms for its production, DNA molecules, process of preparation and use thereof	JOURNAL Patent: BP 0698667-A 10 28-FEB-1996; COMMENT. Other publication BE 1008751 960702 Other publication BE 1008570 960604 Other publication BR 9503454 960305 Other publication PP 953578 960127 Other publication PP 953578 960127 Other publication AU 2508695 960127 Other publication AU 2508695 960127 Other publication AU 2508695 960127 Other publication AU 2508696 960127	ORIGIN Query Match Query Match Query Match Best Local Similarity 100.0%; Score 744; DB 6; Length 1513; Best Local Similarity 100.0%; Pred. No. 1.88-187; Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy ATGAGACAAAGAAATTGACGTTGATTTTAGCTTTTTTTTT	121 TATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGC 191 GGTACGTTCAGTGCAAAGATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGC 191 GGTACGTTCAGTGCCCAATGGAACAATGTTAACAACATATTATTCCGTAAAGGTAAAAAA 800 GGTACGTTCAGTGCCCAATGGAACAATGTTAACAACATATTATTCCGTAAAGGTAAAAAA 241 TTCAATGAAACACAACAACAAGTTGGTAACATGTCCATAAACTAGGAGCCAAC	OY 301 TICCAACAATIGGTAATTATGGGTGTGGACTGGACTGGCCCCTTGTC 360

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1 (Dases 1 to 1513)
De Buyl, E. Lahaye, A., Ledoux, P. and Detroz, R.
Xylanase, microorganisms producing it, DNA molecules, methods for preparing this xylanase and uses of the latter
Patent: US 6346407-A 11 12-FEB-2002;
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1 (bases 2 to 1513)
De Buyl,E., Lahaye,A., Ledoux,P. and Detroz,R.
Xylanase, microorganisms producing it, DNA molecules, methods foreparing this xylanase and uses of the latter
Patent: US 6346407-A 10 12-FEB-2002;
Location/Qualifiers
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WO 9743409-A 1 20-NOV-1997;
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Dalboege, H., Diderichsen, B., Sandal, T. and Kauppinen, S.
METHOD OF PROVIDING NOVEL DNA SEQUENCES
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A68006
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SIKGIATFKQYWSYREKRFGRTIGYSNHFFAMENLGMNMGKMYEVALTVEGYQSSGS
ANVYSNTLRINGNPLSTISNDKSITLDKNN"
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Pred. No. 2.4e-179;
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S Van,S.P., Williams,D.P., Iverson,S., Farrell,R.L., Herbes,W.T., Van,S.P., Williams,D.P., Iverson,S., Farrell,R.L., Herbes,W.T., Van,B.R., Quax,W.J., Goedegebuur,F. and Jones,B.E.
ALKALI-TOLERANT XYLANASES
D PATCHI: WO 9518219-A 18 06-JUL-1995;
GIST BROCADES NV (M.)
Other publication BR 9405934 951226
Other publication BR 9405934 951226
Other publication FI 953920 950811
Other publication FI 953920 950811
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Other publication FI 953920 950811
Location/Qualifiers
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larity 95.7%; Pred. No. 3.9e-168;
Conservative 0; Mismatches 29;
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Sequence 18 from Patent WO9518219.
A45313.1 GI:2299796
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Dalb.o slashed.ge,H., Sandal,T., Kauppinen,M.Sakari. and
Diderichsen,Bslashedrge.
Method of providing a hybrid polypeptide exhibiting an activity interest
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Pred. No. 2.4e-179;
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                                                                                                                                                                                                                                                                            Patent: US 6270968-A 1 07-AUG-2001;
Location/Qualifiers
1.744
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                                                                                       AR163110 744 bp
ARQUENCE 1 from patent US 6270968.
AR163110 GI:16233600
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Best Local Similarity 97.4%;
Matches 725; Conservative
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Unclassified.
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De, B.E., Lahaye, A., Ledoux, P. and Detroz, R.
Xylanase, microorganisms for its production, DNA molecules, process
of preparation and use thereof
Patent: EP 0698667-A 1 28-FEB-1996;
SOLVAX (BE)
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                       178 GGTACGTTCAGTGCCCAATGGAATAATGTTAACAATATATTATTATTCCGTAAAGGTAAAAAAA
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Sequence 1 from Patent EP0698667.
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TTCAATGAAACACAACACCAACAAGTTGGTAACATGTCCATAAACTATGGCGCAAAC 297
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.larity 95.7%; Pred. No. 3.9e-168;
Conservative 0; Mismatches 29;
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/note="unnamed protein product; Protein sequence is in conflict with the conceptual translation"
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/codon_start=1
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100.0%; Pred. No. 7.7e-166;
ive 0; Mismatches 0;
publication CA 2154628 960127
publication AU 2508695 960208.
Location/Qualifiers
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/product="unnamed"
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s. Lahaye, A., Ledoux, P. and Detroz, R.
Xylanase, microorganisms for its production, DNA molecules, process of preparation and use thereof.
Aptent: EP 069867-A 2 28-FEB-1996;
SOLVAY (BE)
Other publication BE 1008751 960702
Other publication BE 8503454 960305
Other publication FP 8903284 960305
Other publication FP 953578 960127
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Sequence 2 from Patent EP0698667.
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Be Buyl, E., Liahaye, A., Ledoux, P. and Detroz, R.
Xylanase, microorganisms producing it, DNA molecules, methods for preparing this xylanase and uses of the latter
Patent: US 6346407-A 1 12-FFB-2002;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 7.7e-166;
Matches 663; Conservative 0; Mismatches 0; Indels
                             linear
                              DNA
                                                                                                                                                                                                                                                     /organism="unknown"
/mol_type="unassigned DNA"
                        Sequence 1 from patent US 6346407.
                                                                       AR193049.1 GI:20239014
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1 ATGAGACAAAAGAAATTGAC......TAACTTTGGATAAAAACAAT 744
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description			_			Aat16101 Xylanase	Aav13074 Xylanase	Adj34947 DNA encod	Adj35051 DNA encod	Adj34969 DNA encod	Aaq80923 B. pumilu	Aaz51821 Clostridi	Aat90972 Nucleotid	Aat08142 Xylanase	Adj35011 DNA encod	Aaq92876 Thermosta	Aaq92875 Thermosta	Adj35101 DNA encod	Adj35151 DNA encod		Adj34999 DNA encod
IES									_		_											_
SUMMARIES	Ĺ	AAT16102	AAT16103	AAV13067	4AV30255	AQ92878	AT16101	AAV13074	ADJ34947	ADJ35051	ADJ34969	AQ80923	AAZ51821	4AT90972	AAT08142	ADJ35011	AAQ92876	AA092875	ADJ35101	ADJ35151	ADJ34965	ADJ34999
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	* Query Match Length DB	744	1513	744	871	744	663	747	1068	1956	684	1022	2364	1190	1244	747	164	164	1695	1338	1077	1065
	Query Match	100.0	100.0	95.9	95.9	90.3	89.1	78.9	52.8	37.2	36.9	36.7	34.4	28.5	27.5	23.9	20.8	20.3	19.3	19.2	18.3	17.5
	Score	744	744	713.6	713.6	671.6	663	587.2	393	276.6	274.4	273	255.6	212.2	204.8	177.8	154.4	151.2	143.6	142.6	136.2	130.2
	Result No.		8	m	4	ß	9	7	- 00	6	10	11	12	13	14	15	16	17	18	19	20	21

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ADJ34949 ADJ34955 AAX90405 AATG4930 AAV15063	AAV36098 AAT42374 ADJ34943 ADJ35083 AAV15059	. ~ ~ ~ ~	4	
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ALIGNMENTS

AT16102 stand	AAT16102 standard; DNA; 744 BP.
AAT16102;	
16-OCT-2003 15-MAY-1996	(revised) (first entry)
Xylanase precursor gene	urbor gene.
Xylanase; the ss.	Xylanase; thermostable enzyme; paper; pulp; bleaching; feedstuff; baking; 88.
Bacillus sp;	strain 710/1 (LMG P-14798).
Key sig_peptide	Ä
mat_peptide	/.cg= a 82. 744 /*tag= b /EC_number= "3.2.1.8"
AU9525086-A.	
08-FEB-1996.	
19-JUL-1995;	95AU-00025086.
26-JUL-1994; 17-MAY-1995;	94BE-00000706. 95BE-00000448.
(SOLV) SOLVAY	Y SA.
De Buyl E, L	Lahaye A, Ledoux P, Detroz R;
WPI; 1996-117341/13 P-PSDB; AAR92054.	341/13. 054.
Bacillus deri of paper pulp	Bacillus derived xylanase active over wide pH range - used in treatment of paper pulp, animal feeds and in bakery goods.
Claim 9; Page	Page 54-55; 94pp; English.

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A DNA sequence (AAT16102) coding for a xylanase precursor (AAR92054) was isolated from a gene library of Bacillus sp. 720/1 (LMG P-14798). The sequence (AAT16103) for the complete gene including 5' and 3' untranslated sequences was also obtd. The gene may be incorporated into a vector and expressed from either its own promoter or from the Bacillus pumilus PRL B12 promoter (see AA073996), and used for profd. of recombinant thermostable xylanase in transformed hosts, pref. Bacillus licheniformis or B. pumilus. The enzyme is useful in the paper-pulp, animal feed and baking industries. (Updated on 16-0CT-2003 to standardise
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                                                                                                                                        Length 744;
                                                                                                                  Sequence 744 BP; 246 A; 144 C; 160 G; 194 T; 0 U; 0 Other;
                                                                                                                                                             Indels
                                                                                                                                       100.0%; Score 744; DB 2; L
100.0%; Pred. No. 1.5e-210;
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                                                                                                                                                              0; Mismatches
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                                                                                                                                                   Best Local Similarity 100.
Matches 744; Conservative
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RESULT 2 AAT16103 ID AAT16103 standard; DNA; 1513

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                                                                            Kylanase; thermostable enzyme; paper; pulp; bleaching; feedstuff; baking;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus derived xylanase active over wide pH range - used in treatment of paper pulp, animal feeds and in bakery goods.
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ilarity 100.0%; Pred. No. 2.1e-210;
Conservative 0; Mismatches n:
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                                                                                                                                                              Location/Qualifiers
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/*tag= a
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                                                                                                                                    strain 710/1 (LMG
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701. .1363
/*tag= d
/EC number= '
1367. .1513
/*tag= e
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95BE-00000448
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/*tag= b
620. .600
/*tag= c
(revised)
(first entry)
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17-MAY-1995;
16-OCT-2003
15-MAY-1996
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an example of the present invention. The present invanious activity used in novel method for providing a novel DNA sequence encoding a polypeptide from a microorganism with an activity of interset. The method comprises: (i) PCR amplification of the DNA with PCR primers with homology to (a) known gene(s) encoding a polypeptide with an activity of interest; (ii) linking the obtained PCR product of a 5' structural gene sequence; (iii) expressing the resulting hybrid DNA sequence; (iv) screening for hybrid DNA sequences encoding a polypeptide with the activity of interest or a related activity; and (v) isolating the hybrid DNA sequence identified in step (iv). This method provides for identification and isolation of sequences from microorganisms without having to cultivate and isolate the microorganism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                661 GTATATAGCAATACACTAAGAATTAACGGTAACCCTCTCTCAACTATTAGTAATGACGAG 720
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                                                                                     present sequence encodes a polypeptide with xylanase activity
                            - without the
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                                                                                                                                                                                                                                                                    Length 744;
                                                                                                                                                                                                                                                Sequence 744 BP; 249 A; 146 C; 157 G; 192 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                             Indels
                             Isolating novel DNA sequences from microorganisms culturing the microorganism.
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Pred. No. 1.7e-201;
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                                                                Example 1; Page 31-32; 72pp; English
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Best Local Similarity
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                                                                                                                                  GAATATTATATTGTCGACAGTTGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGG
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1. .747
/*tag= a
/product= "glycosyl hydrolase family 11 xylanase"
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Xylanolytic enzyme; Bacillus agaradherens NCIMB 40482; breakdown; agricultural waste; alcohol fuel; enzymatic treatment; animal feed; release; free pentose sugar; dissolving pulp; cellulose; bio-bleaching; wood pulp; lignocellulostic material; animal feed additive; ss.
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                                                                   AGCATAACTTTGGATAAAAACAAT
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P-PSDB; AAW60562.
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06-JUN-1995;
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               TATGATTATGAATTTTTGGAAAGATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGC
                                                                                                                       TTCCAACCAAATGGTAATGCGTATTTATGCGTCTATGGTTGGACTGTTGACCCTCTTGTC
AIGAGACAAAAGAAATIGACGTIGATTITIAGCCTTTTTAGTTTTTTGCACTAACCTTA
                                                    CCTGCAGAAATAATTCAGGCACAAATCGTCACCGACAATTCCATTGGCAACCACGATGGC
                                                                    GGTACGTTCAGTGCCCAATGGAACAATGTTAACAACATATTATTCCGTAAAAAAA
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A DNA sequence (AAT16101) coding for a thermostable mature xylanase (AAR92053) was isolated from a gene library of Bacillus sp. 720/1 (LMG P-14798). Sequences were also obtd. (see AAT16102 and AAT16103) for the xylanase precursor and for the complete gene including 5' and 3' untranslated sequences. DNA coding for the mature enzyme may be incorporated into a vector and expressed from either its own promoter or from the Bacillus pumilus PRL B12 promoter (AAQ73996), and used for prodn. of recombinant xylanase in transformed hosts, pref. Bacillus licheniformis or B. pumilus. The enzyme is useful in the paper-pulp, animal feed and baking industries. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                        Xylanase; thermostable enzyme; paper; pulp; bleaching; feedstuff; baking;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus derived xylanase active over wide pH range - used in treatment of paper pulp, animal feeds and in bakery goods.
GTATATAGCAATAACACTAAGAATTAACGGTAACCCTCTCTCAACTATTAGTAATGACGAG
                                                                          GGGAAAATGTATGAAGTCGCGCTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAAT
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/EC number= "3.2.1.8"
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                                                                                                                                                                                                                                                                         Novel xylanase enzyme active at high pH - useful in paper and pulp prodn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGC
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                                                                                                                                                 Herbes WT;
Quax WJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                 Van Solingen P, Williams DP, Iverson S, Farrell RL,
Van Der Kleij WA, Herweijer MA, Van Beckhoven RFWC,
Goedegebuur F, Jones BB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 90.3%; Score 671.6; DB 2; Best Local Similarity 95.7%; Pred. No. 5.1e-189; Matches 712; Conservative 0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 42-43; 54pp; English.
                                              94WO-EP004312
                                                                                  93EP-00203694
                                                                                                                   (KONN ) GIST-BROCADES NV
                                                                                                                                                                                                                            WPI; 1995-246385/32.
                                                                                                                                                                                                                                              P-PSDB; AAR76551
                                              23-DEC-1994;
                                                                                  24-DEC-1993;
             06-JUL-1995
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 /*tag= a
 /product= "positive clone for xylanase activity"

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Diderichsen B,

97WO-DK000216. 96DK-00000562

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novel DNA sequences from microorganisms - without the need the microorganism.
                                                                                                                                                                             Example 1; Page 35; 72pp; English
                                                                                                   (NOVO ) NOVO-NORDISK AS
                                                                                                                                    WPI; 1998-008878/01.
                                                                  12-MAY-1997;
                                                                                   10-MAY-1996;
                                WO9743409-A2
                                                20-NOV-1997.
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                                                                                                                                                                                                                                    441
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                                                                                            GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGG 201
                                                                                                            GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGG 120
                                                                                                                              AACAATGTTAACAACATATTATTCCGTAAAGGTAAAAATTCAATGAAACACAAACACAC 261
                                                                                                                                        CAAATCGTCACCGACAATTCCATTGGCAACACGATGGCTATGATTATGAATTTTGGAAA 60
                                                                                                                                                                                                                                                                                                                                                    TGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGA
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                                                           CAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAA
                                            Gaps
                                            ó
                          Length 663;
          C; 146 G; 166 T; 0 U; 0 Other;
                                           0; Indels
                          tch 89.1%; Score 663; DB 2; L sal Similarity 100.0%; Pred. No. 1.7e-186; 663; Conservative 0; Mismatches 0;
            BP; 220 A; 131
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            Sequence 663
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                                                                                                                                                                                                                                                                                                                                                                                                98;
                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                 Score 587.2; DB 2;
Pred. No. 6.3e-164;
0; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                     Query Match 78.9%;
Best Local Similarity 86.8%;
Matches 646; Conservative
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Bacillus sp; xylanase; glycosyl hydrolase family 11; isolation; microorganism; identification; hybrid DNA; ss.

Location/Qualifiers

Synthetic. Bacillus sp.

Key

Xylanase activity positive clone DNA SEQ ID NO:11

19-MAY-1998 (first entry)

AAV13074;

AAV13074 standard; DNA; 747 BP.

AAV13074

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Sequence 1068
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                      540
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ACCATCACTGTTGACGGGGGGACGTATGATATCTACAAGCACCAACAGGTCAATCAGCCA 480
                                                                                                                                                                                                                                                                                                                                                                                     antibacterial; fungicide; thermostable xylanase activity;
dough conditioning; beverage production; nurritional supplement;
animal feed; lignin reduction; wood product; xylan; bacterial infection;
fungal infection; coccidiosis; gene; ds.
                      TCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGTGTTCGAAGATCGAAACGCACG
                                                                                  GTATATAGCAATACACTAAGAATTAACGGTAACCCTCTCTCAACTATTAGTAATGACGAG
                                                                                                                                                                                  GTATATAGCAATACACTAAGAATTAACGGTAACCCTCTCTCAACTATTAGTAATGACAAG
                                            rcrarrcadegeaccececercrarcagracragicarrearreagageageage
                                                                   AGTGGCACGATTTCTGTCAGCAACCACTTTAGAGCGTGGGAAAACTTAGGGATGAATATG
                                                                                                                GGGAAAATGTATGAAGTCGCGTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAAT
                                                                                                                                      derecarricaarraccagarccrcgrracrdagggcraccaarcraccggaagrcraar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel xylanase recombinant polypeptide useful for improving textile texture, treating paper, eliminating microorganisms.
                                                                                                                                                                                                                                                                                                                                                               DNA encoding xylanase from an environmental sample seq id 163.
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                                                                                                                                                                                                            AGCATAACTTTGGATAAAAACAAT 744
                                                                                                                                                                                                                                AGCATAACTCTAGATAAAAACAAT 744
                                                                                                                                                                                                                                                                                           ADJ34947 standard; DNA; 1068 BP.
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P-PSDB; ADJ34948.
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                                                                                                                                                                                                                                                                                                                       117
                                                                                                                                                                                                                                                                                                                                                               TATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTACGTTCAGTGCCCAATGGAACAATGTTAACAACATATTATTCCGTAAAAGGTAAAAAA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCAATGAAACACAACACCCAACAAGTTGGTAACATGTCCATAAACTACGGAGCCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                         TATGACTATGAATACTGGAAGGACAGC---GGGAATGGAACTATGGTTCTCGGTAGTGGC
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                                                                                                                                                                                         1 ATGAGACAAAAGAAATTGACGTTGATTTTAGCCTTTTTAGTTTTGCACTAACCTTA
                                                                                                                                                                                                                                   Archangchangandangringringcogcarririnacricitrinacgcringcacri
sequence encodes xylanase protein isolated from an environmental
                                                                                                                                                   Gaps
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                                                                                                       Length 1068;
                                                             237 T; 0 U; 0 Other;
                                                                                                                                                 Indels
                                                                                                          Score 393; DB 12;
Pred. No. 3.9e-106;
0; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTATATAGGAATACACTAAGAATTAACGG 689
                                                                  C; 279 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
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                                                                                                          Query Match 52.8%;
Best Local Similarity 75.2%;
Matches 518; Conservative (
                                                                  BP; 303 A; 249
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Best Local Similarity
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        549
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                                                                                                                                                                                                                                                                  ADJ34969;
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                                                                                                                                                                                                                                                                                                                The invention describes an isolated or recombinant polypeptide (I), having 50% or more identity to 190 300-1200 residue amino acid sequences (SI), given in the specification, over a region of 100 or more residues and the polypeptide as thermostable xylanase activity. (I) is useful for dough conditioning, beverage production, as a nutritional supplement in animal feed; reducing lignin in a wood or a wood product; and for eliminating and protecting animals from a microorganism comprising xylan. The polymucleotide (II) encoding (I) is useful for amplifying nucleic acid encoding a polypeptide having a xylanase activity which involves amplifying (II) or its subsequence. (I) is useful for treating and preventing bacterial infection and fungal infection e.g. coccidiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGIGGAIGGCGGIACTIAIGAAAIAIAIGAAACIACCGGGIAAAICAGCCTICCAICGA 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTACTCGCCGGGCGAATAATTTACGACAATGAGACAGGCACACATGGAGGCTACGACTA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rcagcrcriedaaaga---cracegaaaracearraregaacrraaceacegreerrr 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 CAGTGCCCAATGGAACAATGTTAACAACATATTATTCCGTAAAGGTAAAAATTCAATGA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACACAAACACCAACCAACTGGTAACATGTCCATAAACTACGGAGCCAACTTCCAACC 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAATGGTAATGCGTATTTATGCGTCTATGGTTGGACTGTTGACCCTCTTGTCGAATATTA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAcGGAAATTCCTATTTGTGTGTTTACGGTTGGACAAGAAATCCACTGGTTGAATATTA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          369 TATTGTCGACAGTTGGGGGAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 AATAATTCAGGCACAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGAATTTTTGGAAAGATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 TAGTTGTCAATGGAGTAATATCGGTAATGCACTATTTAGAAAAGGGAGAAAATTTAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Gaps
                                                                                                                                                                                                                                        Novel xylanase recombinant polypeptide useful for improving textile texture, treating paper, eliminating microorganisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 12; Length 1956;
                                                                                                                                                   Blum D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1956 BP; 614 A; 384 C; 423 G; 535 T; 0 U; 0 Other;
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Pred. No. 2e-71;
0; Mismatches 209; Indels
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                                                                                                                                                    Hazlewood
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                                                                                                                                                    Callen W, Healey S,
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                                                                                        14-JUN-2002; 2002US-0389299P
                                                           16-JUN-2003; 2003WO-US019153
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                                                                                                                                                                                                   WPI; 2004-099016/10.
                                                                                                                       (DIVE-) DIVERSA CORP
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Best Local Similarity
                                                                                                                                                                                                                  P-PSDB; ADJ35052
 WO2003106654-A2.
                                                                                                                                                    Steer B, Callen
Esteghlalian A;
                              24-DEC-2003
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The invention describes an isolated or recombinant polypeptide (I), CC having 50% or more identity to 190 300-1200 residue amino acid sequences (SI), given in the specification, over a region of 100 or more residues CC and the polypeptide as thermostable xylanase activity. (I) is useful for: dough conditioning; beverage production; as a nutritional supplement in animal feed; reducing lignin in a wood or a wood product; and for animal feed; reducing animals from a microorganism comparising xylan. CC The polynucleotide (II) encoding (I) is useful for amplifying nucleic acid encoding a polypeptide having a xylanase activity which involves amplification of a template nucleic acid with a primer pair capable of amplification of a template nucleic acid with a primer pair capable of complifying (II) or its subsequence. (I) is useful for treating and preventing bacterial infection and fungal infection e.g. coccidiosis.

This sequence encodes xylanase protein isolated from an environmental cc sample.
                                                                                                608
                                                                                                                                                            617
                                                                                                                                                                                                                        609 GTATGAAGTCGCGCTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAATGTATAG 668
                                                                                                                                                                                                                                                                antibacterial; fungicide; thermostable xylanase activity; dough conditioning; beverage production; nutritional supplement; animal feed; lignin reduction; wood product; xylan; bacterial infection; fungal infection; coccidiosis; gene; ds.
498 IGGAACTGCGACATTCCAACAATATTGGAGTGTTCGTACATCCAAGAGAACAACGAAC
                                                                                                GATITCTGTCAGCAACCACTTTAGAGCGTGGGAAAACTTAGGGGATGAATATGGGGAAAAAT
                                                                                                                                                     558 aairatöröricacrgaacaririraaacadregeaaaagaaregecaregearegeraaear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding xylanase from an environmental sample seq id
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Pred. No. 5.8e-71;
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                                                                                                                                                                                                                                                                                                                                                             695
                                                                                                                                                                                                                                                                                                                                                                                                                   GAATGAAATCAGAATAGGTGCAAATCC 704
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                                                                                                                                                                                                                                                                                                                                                             669 CAATACACTAAGAATTAACGGTAACCC
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64.6%;
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(SOLV ) SOLVAY
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                                1 ATGAGACAAAAGAAATTGACGTTGATTTTAGCCTTTTTAGTTTTGCACTAACCTTA
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Gaps
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Mismatches 236; Indels
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Purified xylanase from Bacillus pumilus PRL B12 - esp. produced in transformed Bacillus licheniformis, and related DNA, vectors, etc., used for pre-treatment of wood pulp to reduce chlorine or ozone consumption in subsequent bleaching.
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Pred. No. 1.8e-70;
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/EC_number= "3.2.1.8"
/note= "claim 10"
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Best Local Similarity 63.4%;
Matches 452; Conservative
                     186. .869
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                                                                                                                                                                                                                                                                                                                   Xylanase A; XynA; cellulosome; feruloyl esterase; phenolic acid esterase;
thermostable; ferulic acid; wheat bran, agricultural byproduct; treat;
grass; paper and pulp industry; feed processing; food additive;
plant cell wall material; degradation; ds.
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                                                                                                                                    TCATTTTATGCCGATGGAGGCACATATGACATATAGAAACGCTCCGTGTCAATCAGCCT
                                         TCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGTGTTCGAAGGATCGAAACGCACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    546 CACGATITICIGICAGCAACCACTITAGAGCGIGGGAAAACTITAGGGAIGAATATGGGGAA 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATGTATGAAGTCGCGCTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAATGTATA 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            816
material. The novel feruloyl esterase is thermostable, easy to purify, has high temperature optima and stable over a wide pH range. The enzyme is used for producing ferulic acid from wheat bran or agricultural byproducts, treating grasses or other plant materials used in the pulp and paper industries, in feed processing and as a food additive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           xynB gene; xylanse; enzyme; Dictyoglomus thermophilum strain Rt46B.1; G-Xylanase; beta -1,4-xylanase activity; activity; thermal stability; biological bleaching; cellulose product; paper pulp; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAGTTGTCAATGGAGTAATACGGTAATGCACTATTTAGAAAAGGGAGAAAATTTAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369 TATTGTCGACAGTTGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATAATTCAGGCACAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTA
                                                                                                                                                                                                                                                                                                                                                           TGAATTTTGGAAAGATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reaccicregalada --- cracegalaracarrategal ciralegales escretir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGTGCCCAATGGAACAATGTTAACAACATATTATTCCGTAAAAGGTAAAAATTCAATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACACAAACACACCAACAAGTTGGTAACATGTCCATAAACTACGGAGCCAACTTCCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cgacałałakctarcałgałatrakgagakcaracragirgartargartackart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAATGGTAATGCGTATTTATGCGTCTATGGTTGGACTGTTGACCCTCTTGTCGAATATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TG---TIGAIGGAGGAACATAIGAIAICIACGAGACTCTIAGAGICAAICAACCCICCAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAAGGGGATTGCCACATTTAAACAATATTGGAGTGTTCGAAGATCGAAAACGCACGAGTGG
                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                             Length 2364;
                                                                                                                                                          Sequence 2364 BP; 791 A; 428 C; 458 G; 687 T; 0 U; 0 Other;
                                                                                                                                                                                                                DB 3;
                                                                                                                                                                                                                                                                   0; Mismatches 214;
                                                                                                                                                                                                                Score 255.6; DB 3
Pred. No. 3.8e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAGAATGAAATCAGAATAGGTGCAAATCC 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAGCAATACACTAAGAATTAACGGTAACCC 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; DNA; 1190
                                                                                                                                                                                                                34.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dictyoglomus thermophilum
                                                                                                                                                                                                                     Query Match
Best Local Similarity 65.1
Matches 410; Conservative
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680

620 623

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gene was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A full-length xynD gene (AAT08142) codes for a thermostable G-type xylanase (AAR87012) useful in the pulp and paper industries. The gene was obtd. by genomic walking PCR of DNA from an extremely thermophilic bacterium, strain TG456 (CBS 213.94), isolated from a New Zealand hot spring. He gene can be inserted into a vector and used for the produce recombinant xylanase D in microbial host cells, esp. Escherichia coli. (Updated on 25.MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel xylanase(s) having activity at 80 deg.C. or higher - obtained from anaerobic thermophilic bacteria and used in paper and pulp production
                                                                                                             621 TCACTTTAGGGCATGGGCAATAGAGGTTTAAACCTTGGTACTATTGATCAAATTACTCT
                                 TAAACAATATTGGAGTGTTCGAAGATCGAAAACGCACGAGTGGCACGATTTCTGTCAGCAA
                                                                             CCACTTTAGAGCGTGGGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                            TACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAATGTATATAGCAATAC 674
                                                                                                                                                                enzyme; paper; pulp; lignin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

27.5%; Score 204.8; DB 2; Length 1244;
Best Local Similarity 61.0%; Pred. No. 3.6e-50;
Matches 367; Conservative 2; Mismatches 224; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moody D;
Quax WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1244 BP; 380 A; 215 C; 279 G; 360 T; 0 U; 10 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Forster S,
Morgan HW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Iverson S,
Daniel RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Xylanase D; xynD gene; thermostable endelignification; xylan; bleaching; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 9; Page 56-58; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .1107
                                                                                                                                                                                                                                                                    AAT08142 standard; DNA; 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95WO-EP002299.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams DP,
                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Groenberg V, Williams DP,
Farrel RL, Bergquist PL,
Herweijer MA, Jones BE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KONN ) GIST-BROCADES BV.
                                                                                                                                                                                                                                                                                                                                     (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-049690/05.
                                                                                                                                                                                                                                                                                                                                                                                                            gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAR87012
                                                                                                                                                                                                                                                                                                                                                                                                            Xylanase xynD
                                                                                                                                                                                                                                                                                                                                   27-AUG-2003
25-MAR-2003
12-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9534662-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         processes.
                                                                                                                                                                                                                                                                                                       AAT08142;
                                                                                564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria.
               504
                                                                                                                                                  624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263
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                                                                                                                                                                                                                                                                                                                                                                                                            Dictyoglomus thermophilum xylanase gene - used for producing thermally stable enzymes for the bleaching of cellulase products, especially paper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 TAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCAATGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAATGTTAACAACATATTATTCCGTAAAAGTAAAAAATTCAATGAAACACAAAACACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAATATAAACAATGCATTATTCAGAACAGGTAAGAAGTACAAC-----CAAAACTGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCATTAGGCACTATTAGAATCACCTACTCAGCCACATATAATCCTAATGGTAACTCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTATGCGTCTATGGTTGGACTGTTGACCCTCTTGTCGAAATATTATATTGTCGACAGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   444 ATATGATATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

28.5%; Score 212.2; DB 2; Length 1190;
Best Local Similarity 62.4%; Pred. No. 2.2e-52;
Matches 369; Conservative 0; Mismatches 213; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1190 BP; 386 A; 197 C; 277 G; 330 T; 0 U; 0 Other;
                                   /*tag= a
/product= "xylanase"
67. .138
Location/Qualifiers
57. .1149
                                                                                                                                                                                                                                                                                                                           Morris D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 3; 34pp; English.
                                                                                                                                                                                                                          97WO-NZ000042
                                                                                                                                                                                                                                                        96NZ-00286296
                                                                                                                                                                                                                                                                                         (PACI-) PACIFIC ENZYMES LTD
                                                                    67. .138
/*tag= b
139. .1146
/*tag= c
                                                                                                                                                                                                                                                                                                                           Gibbs MD,
                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-503090/46.
                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAW30267.
                                                                                                                                                                                                                                                                                                                           Bergquist PL,
                                                                                                                                                                                                                          27-MAR-1997;
                                                                                                                                                                                                                                                           29-MAR-1996;
                                                                                                                                                       WO9736995-A2
                                                                                                                                                                                       09-OCT-1997.
                                                                      sig_peptide
                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210
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useful for improving textile

nt polypeptide useful for im eliminating microorganisms.

Novel xylanase recombinant

2004-099016/10.

Esteghlalian A;

P-PSDB; ADJ35012

treating paper,

texture,

Claim 1; SEQ ID NO 227; 570pp; English

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388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGAAGGYTACCARAGCAGCGGCTCAGCAAATATAACACAGAATACATTTACTATTGGTG
TCACCGACAATTTCCATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAAGATAGCG
                                                                        rnaccronariscaacrissaanacsarissariacriacriacsastristissaassaassas
                                                                                                                                                    GTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGGAACAATG
                                                                                                                                                                                                                             GGAATACT - - ACCATGACAGTTGACACAGGAGGAGGATTTAGCTGTCAGTGAGTAACA
                                                                                                                                                                                                                                                                                                         TTAACAACATATTATTCCGTAAAAGGTAAAAATTCAATGAAACACAAAAACACAACAAGAG
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antibacterial; fungicide; thermostable xylanase activity; dough conditioning; beverage production; nutritional supplement; animal feed; lignin reduction; wood product; xylan; bacterial infection; fungal infection; coccidiosis; gene; ds.
                                                           DNA encoding xylanase from an environmental sample seq id
 BP.
 ADJ35011 standard; DNA; 747
                                        (first entry)
                                        22-APR-2004
                    ADJ35011;
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Callen W, Healey S, Hazlewood G, 2003WO-US019153 2002US-0389299P. (DIVE-) DIVERSA CORP 16-JUN-2003; 14-JUN-2002; Steer B,

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                                                                                                                                                                    The invention describes an isolated or recombinant polypeptide (I), having 50% or more identity to 190 300-1200 residue amino acid sequences (S1), given in the specification, over a region of 100 or more residues and the polypeptide as thermostable xylanase activity. (I) is useful for dough conditioning; beverage production; as a nutritional supplement in animal feed; reducing lighin in a wood or a wood product; and for eliminating and protecting animals from a microorganism comprising xylan. The polynucleotide (II) encoding (I) is useful for amplifying nucleic amplification of a template mathing a xylanase activity which involves amplifying (II) or its subsequence. (I) is useful for treating and preventing bacterial infection and fungal infection e.g. coccidiosis. This sequence encodes xylanase protein isolated from an environmental sample.
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Matches 257; Conservative
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| /cgn2 6/ptodata/1/ina/5A COMB.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd
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28 255 34.3 600 4 US-09-076-677-34 Sequence 34, Appl 29 255 34.3 600 4 US-09-073-055-26 Sequence 26, Appl 31 204.8 27.5 1244 3 US-09-073-055-24 Sequence 12, Appl 32 154.4 20.8 164 3 US-08-59.1-615 Sequence 12, Appl 32 154.4 20.8 164 3 US-08-59.1-615 Sequence 15, Appl 34 132.4 17.8 294 4 US-09-679-154-4 Sequence 16, Appl 36 119.4 16.0 1775 2 US-08-817-946-4 Sequence 16, Appl 37 119.4 16.0 1775 3 US-08-59.563-1 Sequence 1, Appl 39 119.4 16.0 1775 4 US-09-53-1 Sequence 1, Appl 4 16.0 1775 3 US-08-59.563-1 Sequence 1, Appl 4 16.0 1775 3 US-08-59.563-1 Sequence 1, Appl 4 16.0 1775 3 US-09-770-621-1 Sequence 1, Appl 4 16.0 1775 3 US-09-18-18 Sequence 1, Appl 4 16.0 1775 3 US-09-18-18 Sequence 1, Appl 4 16.0 1775 3 US-09-18-18 Sequence 1, Appl 4 16.0 1775 4 US-09-770-621-1 Sequence 1, Appl 4 16.0 1775 4 US-09-770-621-1 Sequence 1, Appl 4 16.0 1775 2 US-09-770-18 Sequence 18, Appl 4 17.8 15.8 1207 1 US-08-773-964-2 Sequence 2, Appl 4 117.8 15.8 1207 2 US-08-575-564-2 Sequence 2, Appl 4 117.8 15.8 1207 2 US-08-963-500-2 Sequence 49, Appl 45 115.2 15.5 213 3 US-09-189-0608-49 Sequence 49, Appl
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ALIGNMENTS

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RESULT 1

US-08-470-953A-4

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US-08-470-953A-4

Sequence 4, Application US/08470953A

PATEURANT NO. 5454A-1

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                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Plan PC Compatible
CORRANG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,953A
FILING DATE: 6-OCTOBER-1995
CLASSIFICATION: DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELEFAN: (202) 293-1850
TELEFAX: (202) 293-1850
TELEFAX: (202) 293-1850
TELEFAX: (202) 293-1850
   2000 K St., N.W., Suite 200
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ilarity 100.0%;
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ORIGINAL SOURCE:
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LENGTH: 744 base pairs
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                           CITY: Washington STATE: D.C.
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; LOCATION:
US-08-470-953A-5
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| Sequence 5, Application US/08470953A
| Patent No. 6346407
| GENERAL INCPARATION:
| APPLICANT: PIERE LEBOUX
| APPLICANT: RENE DETOUX
| APPLICANT: RENE DETOUX
| TITLE OF INVENTION: Xylanase, microorganisms produced it,
| TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase
| TITLE OF INVENTION: and uses thereof
| TITLE OF INVENTION: ADDRESS:
| NUMBER OF SEQUENCES: 29
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: WILLIAN BRINKE UNITED TO THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE
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                                 Length 744;
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                              Score 744; DB 3;
Pred. No. 9e-223;
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                                                                                                                                       Length 1513;
                                                                                                                                          100.0%; Score 744; DB 3; I
100.0%; Pred. No. 1.3e-222;
                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCATAACTTTGGATAAAAACAAT 1363
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Patent No. 6346407

GENERAL INFORMATION:

APPLICANT: ANDREE LAHAYE

APPLICANT: ERIC DE BUYL

APPLICANT: PIERRE LEDOUX

APPLICANT: RENE DETROZ
                                   MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Bacillus
US-08-470-953A-10
                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 744; Conservative
single
                     linear
STRANDEDNESS:
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APPLICAMY: BAINER LAHAYE
APPLICAMY: BRINE BE BUYL
APPLICAMY: RERE DE BUYL
APPLICAMY: RERE DETROR
APPLICAMY: RERE DETROR
APPLICAMY: RERE DETROR
TITLE OF INVENTION: Xylanase, microorganisms produced it,
TITLE OF INVENTION: Xylanase, microorganisms produced it,
TITLE OF INVENTION: MA molecule, processes for preparation of this xylanase
TITLE OF INVENTION: BAINES HOPER CLISON & LIONE
STREET: 2000 K St. N. W., Suite 200
CORRESPONDENCE ADDRESS:
ADDRESSES: MILLIAN RRINKS HOPER GLISON & LIONE
STREET: 2000 K St., N. W., Suite 200
CONFITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2000 K St., N. W., Suite 200
COMPUTER: BAINES FORM:
MEDIUM TYPE: RADABLE FORM:
MEDIUM TYPE: RADABLE FORM:
MEDIUM TYPE: PALCATION: 135
COMPUTER: BAINES FORM:
MARINES PREADER: PALCATION AND ATA:
APPLICATION NUMBER: US/08/470, 953A
FILING DATE: G-OCTOBER-1995
CLING DATE:
ATTOREY APPLICATION DATA:
APPLICATION NUMBER: 37, 136
REGESTRANTON NUMBER: 37, 136
REFERENCE JOCKET NUMBER: 37, 136
RETREENCE JOCKET NUMBER: 37, 136
RETROOME CHARACTERISTICS: 37, 136
RETREENCE JOCKET JOCKET JOCKET JO
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                            GAATATTATATTGTCGACAGTTGGGGCAACTGGCGTCCACCACGAGGAGCAACGCCTAAGGGG
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860 TICAATGAAACACAAACACCAACCAAGTTGGTAACATGTCCATAAACTACGGAGCCAAC 919
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                                                    TTCCAACCAAATGGTAATGCGTATTTATGCGTCTATGGTTGGACTGTTGACCCTCTTGTC
                                                                                    361 GAATATTATATTGTCGACAGTTGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAAGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09189060B
| Patent No. 6270968
| GENERAL INFORMATION:
| APPLICANT: Bandal, Thomas
| APPLICANT: Sandal, Thomas
| APPLICANT: Rauppinen, Markus
| APPLICANT: Rauppinen, Markus
| APPLICANT: Borge, Diderichsen
| TITLE OF INVENTION: Method Of Providing No. 627/
| FILE REFERENCE: 4772.204 US
| CURRENT APPLICATION WUMBER: US/09/189,060B
| CURRENT PILING DATE: 1988-11-10
| PRIOR FILING DATE: 1997-05-12
| NUMBER OF SEQ ID NOS: 74
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 1
| LENGTH: 744
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Best Local Similarity 97.4%;
Matches 725; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (1)
US-09-189-060B-1
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       Xylanase, microorganisms produced it,
DNA molecule, processes for preparation of this xylanase
and uses thereof
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                                                                                                                                                                                                                                                   COMPUTE: ......

ZIF: 2006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,953A
FILING DATE: 6-OCTOBER-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 4121-40
FILING DATE:
FILING DATE: 737,136
FILING DATE: 737,136
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FILING DATE: 737,136
FILING DATE: 737,136
FILING DATE
                                                                                  NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSER: WILLIAN BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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620..700
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LOCATION: 620..1363
               TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN: Bacillus
                                                                                                                                                                                                                                           COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
FEATURE:
NAME/KEY:
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LOCATION:
US-08-470-953A-11
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 713.6; DB 1;
Pred. No. 3.2e-213;
0; Mismatches 19;
   FILING DATE: 15 AUGUEL 1330
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/470,398
FILING DATE: 06-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/343,600
FILING DATE: 30-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK93/00218
FILING DATE: 2-JUL-92
ATTORNEY/AGENT INFORMATION:
NAME: GLEGG, Valeta A.
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 35,127
RECECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0298
INFORMATION FOR SEQ ID NO: 1:
CELEBRANCE CHARACTER.ESTICS:
LENGTH: 811 DASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Bacillus agaradherens
STRAIN: NCIMB 40482
                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uvery match 95.9%;
Best Local Similarity 97.4%;
Matches 725; Conservative (
                                                                                                                                                                                                                                                                                                                                                  LENGTH: 871 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
82..744
                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: line MOLECULE TYPE: D ORIGINAL SOURCE:
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US-08-698-978-1
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CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5770424ch America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUWTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                     420
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                                                                                                                                                                                                                                                                                                      361 GAATATTATATTGTCGATAGTTGGGGCAACTGGCGTCCACCAGGGGAACGCCTAAGGGA
                                                                                                                                                                                                                                                                                                                                                                        TATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGC
                      TATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGC
                                                                  GGTACGTTCAGTGCCCAATGGAACAATGTTAACAACATATTATTCCGTAAAAGGTAAAAAA
                                                                                                  GGTACGTTCAGTGCCCAATGGAACAATGTTAACAACATATTATTCCGTAAAGGTAAAAAA
                                                                                                                                     TTCAATGAAACACAAACACCAACAAGTTGGTAACATGTCCATAAACTACGGAGCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08698978
Parent No. 5770424
GENERAL INFORMATION:
APPLICANT: Outrrup, Helle
APPLICANT: Dambmann, Claus
APPLICANT: Olsen, Arne Agerlin
APPLICANT: Bisg rd-Frantzen, Henrik
APPLICANT: Jorgensen, Per Lina
APPLICANT: Jorgensen, Per Lina
TITLE OF INVENTION: DNA CONSTRUCTS AND METHODS OF PRODUCING
TITLE OF INVENTION: XLANOLYTIC ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPARE: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/698,978
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US-08-698-978-1
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Sequence 1, Application US/08470953A

Sequence 1, Application US/08470953A

GENERAL INFORMATION:
APPLICANT: ANDREE LAHAYE
APPLICANT: RELC DE BUYL
APPLICANT: PIERRE LEDOUX
ITLE OF INVENTION: Xylanase, microorganisms produced it,
TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase;
TITLE OF INVENTION: and uses thereof
NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    541 AGTGGCACGATTTCTGTCAGCAACCACTTTAGAGCGTGGGAAAACTTAGGGATGAATATG 600
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                                                                                                                                                                                                                                                                            3;
                                Length 744;
                                                                   Indels
                                                                                                         1 ATGAGACAAAAGAAATTGACGTTGATTTTAGCCTTTTTAGTT
                              Score 671.6; DB 3;
Pred. No. 4e-200;
0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              744
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                                / Match 90.3%;
Local Similarity 95.7%;
nes 712; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-470-953A-1
US-08-501-126-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 2000 Feminary......
CITY: Washington
STATE: DOUG-1812
COUNTRY: USA
ZIP: 2006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,126
FLING DATE: 29-DEC-1995
CLASSIFICATION: 425
ATTORNEY/AGENT INFORMATION:
NAME: WULTSAHIGE, Kate H.
REGISTRATION NUMBER: 29,559
REPRENCE/DOCKET NUMBER: 29,559
REPRENCE/DOCKET NUMBER: 4615-0057.00
TELECPMA: (202) 887-1500
TELECPMA: (202) 887-1500
TELECPMA: (202) 887-1503
INFORMATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDESS: double
TYPE: DIAGY: linear
MOTECTILE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Van Solingen, Pieter
APPLICANT: Van Solingen, Diane P.
APPLICANT: Iverson, Sara
APPLICANT: Farrell, Roberta L.
APPLICANT: Herbes, Wilhelmina T.
APPLICANT: Herbes, Wilhelmina T.
APPLICANT: Van Der Kleij, Wilhelmus A.
APPLICANT: Van Beckhoven W.C., Rudolf F.
APPLICANT: Quax, Wilhelmus J.
APPLICANT: Quax, Wilhelmus J.
APPLICANT: Quax, Wilhelmus J.
APPLICANT: ALKALI-TOLERANT XYLANASES
NUMBER OF SEQUENCES: 20
CORRESPONDER ADBRESS:
CORRESPONDER ADBRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1..744
OTHER INFORMATION: /product= "xylanase"
                                                                                                                                                                                                                        721 AGCATAACTTTGGATAAAAACAAT 744
                                                                                                                                                                                                                                                         AGCATAACTCTAGATAAAAACAAT 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue,
                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/08501126
Patent No. 6140095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CBS672.93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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NAME/KEY: CDS
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ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                  US-08-501-126-18
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Sequence 2, Application US/08470953A
Patent No. 6346407
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ENTE DE BUYL
APPLICANT: PIERRE LEDOUX
APPLICANT: PIERRE LEDOUX
APPLICANT: PIERRE LEDOUX
APPLICANT: PIERRE LEDOUX
APPLICANT: PIERRE LEDOUX
APPLICANT: PIERRE LEDOUX
APPLICANT: RENE DETROZ
TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase;
TITLE OF INVENTION: and uses thereof
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSES: WILLIAN BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
                                                                                                                                                                                                                                                                                                                       621
                                                                                                                                     CTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAATGTATATAGCAATACACTAAGA 681
                                                                                                                                                                             562 AACCACTTTAGAGCGTGGGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCG
                                       SITATE: D.C.

ZIP: 20006

COUNTRY: U.S.A.

ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OFFWARE: Patentin Release #1.0, Version #1.25

SOFFWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,953A

FILING DATE: 6-COTOBER-1995

CLASSIFICATION NUMBER: US/08/470,953A

PILING DATE: G-COTOBER-1995

FILING DATE: G-COTOBER-1995

FILING DATE: G-COTOBER-1995

REGISTRATION NUMBER: 37,136

REGISTRATION NUMBER: 37,136

REGISTRATION NUMBER: 37,136

RECECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625

TELEPHONE: 202-429-0625

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MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                        742 AAT 744
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; LOCATION:
US-08-470-953A-2
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US-08-470-953A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTAAACAATATTGGAGTGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGC 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 CAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGG 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAA
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                                                                                                                                                                  CUMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: Perentin Release #1.0, Version #1.25
CUMBENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,953A
FILING DATE: 6-OCTOBER-1995
CLASSIFICATION NUMBER: US/08/470,953A
FILING DATE: #135
APPLICATION NUMBER: US/08/470,953A
FILING APPLICATION NUMBER: US/08/470,953A
ATTORNEY/AGENT INFORMATION:
FILING DATE: ADMINER: 37,136
FILING DATE: WINDER: 37,136
FILING DATE: WINDER: 37,136
FILING DATE: TOO-429-0625
FELEPHONE: 202-429-0625
FELEPHONE: 202-4
                  3: WILLIAN BRINKS HOFER GILSON & LIONE 2000 K St., N.W., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Bacillus
                                                  STREET: 2000 K St
CITY: Washington
STATE: D.C.
                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 20006
                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-470-953A-1
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TYPE: DNA ORGANISM: Hybrid FEATURE:
                                                                   NAME/KEY: CDS
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                                                                                                                                 1 CABATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGGAATTTTTGGAAA
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                                                                                                                                                                                                142 GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGG
                                                                                                                                                                                                                                                                                        TATTTATGCGTCTATGGTTGGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGT
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                       Length 663
                                                              Indels
                Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e-197;
Matches 663; Conservative 0; Mismatches 0;
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US-09-189-060B-11
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                                                     Score 587.2; DB 3;
Pred. No. 1e-173;
0; Mismatches 98;
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GENERAL INFORMATION:
APPLICANT: DE BUYL, ERIC
APPLICANT: LAHENE, ANDR E
APPLICANT: LEDOUX, PIERRE
APPLICANT: AMORY, ANTOINE
                                                       78.9%;
86.8%;
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LEDOUX, PIERRE
AMORY, ANTOINE
                                                     Query Match 78.9
Best Local Similarity 86.8
Matches 646; Conservative
... (744)
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US-09-189-060B-11
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US-08-275-526C-1
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ZIP: 20006
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/275,526C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 35, Application US/08275526C Patent No. 6180382
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TELEFAX: (202) 293-0625
TELEX: 650 383 5605
INFORMATION FOR SEQ ID NO: 35:
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GENERAL INFORMATION:
APPLICANT: DE BUYL, ERIC
APPLICANT: LAHAYE, ANDR E
APPLICANT: LEDOUX, PIERRE
APPLICANT: AMORY, ANTOINE
APPLICANT: AMORY, ANTOINE
APPLICANT: AMORY, REW
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ATTORNEY/AGENT INFORMATION:
NAME: Gadiano, Wilhlem F.
REGISTRATION NUMBER: 37,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: genomic DNA
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LENGTH: 1022 base pairs
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STRANDEDNESS: single
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TITLE OF INVENTION:
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                                                                                                   XYLANASE DERIVED FROM A BACILLUS SPECIES,
EXPRESSION VECTORS FOR SUCH XYLANASE AND
COTHER PROTEINS, HOST ORGANISMS THEREFOR AND
USE THEREOF
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2.4e-75;
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                                                                                                                                                                                                       STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 15-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRERENCE/DOCKET NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 37,136
RETERRENCE/DOCKET NUMBER: 37,136
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (202) 429-0625
TELEPAX: (202) 439-6625
TELEPAX: (202) 393-6625
TELERENCE CARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 255;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOCTWARE: Patentin n.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Bacillus pumilus
STRAIN: PRL B12
                                            CHRISTOPHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.78;
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Best Local Similarity 63.4%;
Matches 452; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: genomic DNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1022 base pairs
                                      APPLICANT: ANDRE, CHRISTAPLICANT: VETTER, ROMALITLE OF INVENTION: XYLLTILE OF INVENTION: OTHITLE OF INVENTION: OTHITLE OF INVENTION: USE NUMBER OF SEQUENCES: 35 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              20006
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                                                                                                                                                                             Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 273; DB 4;
Pred. No. 2.4e-75;
                                                                                                                                                                                               CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/09/076,677
FILING DATE: 12-May-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/275,526
                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                              FILING DATE: 15-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gadiano, Wilhiem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-49
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN: PRL B12
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Bacillus pumilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-0625
TELEX: 650 383 5605
INFORMATION FOR SEQ ID NO: 1:
                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: genomic DNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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ilarity 63.4%;
Conservative
                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1022 base
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
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Best Local Simil
Matches 452; C
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                                                                                                                                     186 ATGAATTTGAAAAGATTGAGGCTGTTGTTTTGTGTGTTTTGGATTTTGTGCTGACACTG 245
                                                                                                                                                                               CCTGCAGAAATAATTCAGGCACAAATCGTCACCGACAATTCCATTGGCAACCACGATGGC 120
                                                                                                                                                                                                                                                                       TATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGC 180
                                                                                                                                                                                                                                                                                                                                                            GGTACGTTCAGTGCCCAATGGAACAATGTTAACAACATATTATTCCGTAAAGGTAAAAAA 240
                                                                                                                                                                                                                                                                                                                                                                                                      GGGGCATTTAGTGCAAGCTGGAACAATATTGGAAATGCCTTATTTCGAAAAGAAGAAG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TICAAIGAAACACAAAACACCAACAAGIIGGIAACAIGICCAIAAACIACGGAGCCAAC 300
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                                                                                                                                                                                                                           246 ACGGCTGTGCCGGCTCATGCGGAAACGATTTATGATAGGATAGGGACACACAGGGA 305
                                                                                                                                                                                                                                                                                                              raccaritricaaritariccaaccaritacccaaraaraccrcc---arcacacrcaaraacccc 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rrrgarrccacraaaacrcarcarcaacriggcaacarcrccarcaacracaacgcagcc 482
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CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
  Length 1022
  Score 273; DB 3; Length 10 Pred. No. 2.4e-75; 0; Mismatches 255; Indels
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Patent No. 6423523
GENERAL INPORMATION:
APPLICANT: DE BUYL, ERIC
LAHAYE, ANDREE
LEDOUX, PIERRE
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DETROZ, RENE
ANDRE, CHRISTOPHE
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US-09-076-677-1
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US-09-073-055-1
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                                                                     AGTGGCACGATTTCTGTCAGCAACCACTTTAGAGCGTGGGAAAACTTAGGGATGAATATG
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                                                                                                                                                                                                                                                                                                                   APPLICANT: DE BUYL, ERIC
LAHAYE, ANDREE
LEDOUX, PIERRE
AMORY, ANTOINE
DETROZ, RENE
ANDRE, CHRISTOPHE
VETTER, ROWAN
TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: WILLIAN BRINKS HOPER GILSON & LIONE,
STREET: 2000 K St., N.W., Suite 200
CITY Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/076,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/275,526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Gadiano, Wilhlem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 12-May-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 15-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                              Sequence 35, Application US/09076677 Patent No. 6423523 GENERAL INFORMATION:
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TELEX: 650 383 5605
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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ZIP: 20006
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EXPRESSION VECTORS FOR SUCH XYLANASE AND
COTHER PROTEINS, HOST ORGANISMS THEREFOR AND
USE THEREOF
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CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE,
STREET: 2000 K St., N.W., Suite 200
  Indels
  Mismatches 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMORY, PIERRE AMORY, ANTOINE DETROZ, REN
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                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,055
FILING DATE: OS-May-1998
CLASSIFICATION: <unimal column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column column
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PRIOR APPLICATION NUMBER: US/08/275,526
FILING DATE: 15-UUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gadiano, wilhlem F.
REGISTRATION NUMBER: 37,136
REFERENCE/COCKET NUMBER: 4121-49
TELECOMMUNICATION INFORMATION:
TELEPAX: (202) 293-0625
TELEFAX: (202) 293-0625
TELEFAX: (202) 293-0625
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRACTERISTICS:
LENGTH: 1022 base pairs
TYPE: NUCleic acid
STRATE NUCLEIC acid
STRATE NUCLEIC acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bacillus pumilus
;
STRAIN: PRL B12
;
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-073-055-1
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MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
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601 GGGAAAATGTATGAAGTCGCGCTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAAT
                                                                                                                                                                                                                            780 GGAAAAATGTATGAAACAGCATTAACTGTAGAAGGCTACCGAAGCAACGGAAGTGCGAAT
                                                                             541 AGTGGCACGATTTCTGTCAGCAACCACTTTAGAGCGTGGGAAAACTTAGGGATGAATATG
                                                                                                                                                                                                                                                                                    661 GTATATAGCAATACACTAAGAATTAACGGTAACCCTCTCTCAACTATTAGTAA 713
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cch completed: November 11, 2004, 01:34:20 time : 86.4689 secs

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November 10, 2004, 21:26:43; Search time 475.684 Seconds (without alignments) 8421.106 Million cell updates/sec
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1 ATGAGACAAAAGAAATTGAC......TAACTTTGGATAAAAACAAT 744
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1: /cgn2 6/ptodata/1/pubpna/USO7 PUBCOMB.seq:*
2: /cgn2 6/ptodata/1/pubpna/PCT NEW PUB.seq:*
3: /cgn2 6/ptodata/1/pubpna/USO6 NEW PUB.seq:*
4: /cgn2 6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
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8: /cgn2 6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
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11: /cgn2 6/ptodata/1/pubpna/USO9E_PUBCOMB.seq:*
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18: /cgn2 6/ptodata/1/pubpna/USOOE_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3611042 segs, 2692057975 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                              - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-909-207-4
                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                              OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 4, Appli	Sequence 5, Appli	Sequence 10, Appl	Sequence 11, Appl	Sequence 1, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 39, Appl		Sequence 70, Appl	Sequence 68, Appl	
SUMMARIES	ID	US-09-909-207-4	US-09-909-207-5	US-09-909-207-10	US-09-909-207-11	US-09-909-207-1	US-09-909-207-2	US-09-770-621-1	. US-10-286-993-1	S US-10-307-441-39	US-10-213-990-71	US-10-213-990-70	US-10-213-990-68	
	1 DB	6	5	<u>ه</u>	6	6	٥ -	0	15	15	14	14	. 14	
	% Query Match Length DB	744	744	1513	1513	663	663	1375	1375	596	942	1002	705	
	& Query Match	100.0	100.0	100.0	100.0	89.1	89.1	16.0	16.0	15.5	15.0	14.8	14.6	
	Score	744	744	744	744	663	663	119.4	119.4	115.2	111.4	110	108.8	
		1				_				_	_			

Result No.

APPLICATION NUMBER: 08/470,953
FILING DATE: 06-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F' Gadiano, Esq.
REGISTRATION NUMBER: 37,136

Sequence 1, Appli	64,	65,	67,	m	ģ	~	ä	Ξ	Ξ	H	H	ທັ	<u>-</u>	œ	Sequence 9, Appli		φ,	Sequence 3, Appli	Ä	4.	Sequence 8, Appli	-ì	82	Sequence 37173, A	_	ດັ	Sequence 1, Appli	n.	ň	~	1, Ap	Sequence 31, Appl
5 US-10-299-393-1	4 US-10-213-990-64	4 US-10-213-990-65	OS	0 US-09-803-454-3	ns	ns	5 US-10-237-386-10								US-10-244-59	US-09-909-207-7	US-09-909-207-8							US-10-425-115-371	18 US-10-425-115-177283			US-10-419-969-5	S US-10-340-860A-39		US-09-970-616-1	1 US-09-149-310-31
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14.2	14.1	13.9	13.0	11.7	11.3	11.3	11.2	11.2	11.1	11.1	11.1	11.1	11.1	11.1	11.1	10.9	10.9	10.9	10.9	10.7	10.6	10.5	10.4	10.2	6.6	7.6	7.6	7.3	6.8	5.5	5.4	5.4
106	104.8	103.6	96.8	86.8	84.2	84	83.2	83.2	82.6	82.6	82.6	82.6	82.6	82.6	82.6	81	81	81	81	79.4	79	77.8	77.2	75.8	73.8	72.4	72.4	54.2	50.4	41	40	40
13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

TITLE OF INVENTION: Xylanase, microorganisms produced it,

DNA molecule, processes for preparation of this xylanase
and uses thereof CORESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE STREET: 2000 K St., N.W., Suite 200
CITY: Washington STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ish PC compatible
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
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COMPUTER: Ploppy disk
COMP APPLICATION NUMBER: US/09/909,207 FILING DATE: 19-Jul-2001 CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA: Sequence 4, Application US/09909207 Patent No. US20020115181A1 GENERAL INFORMATION: ERIC DE BUYL PIERRE LEDOUX RENE DETROZ APPLICANT: ANDREE LAHAYE NUMBER OF SEQUENCES: 29 RESULT 1 US-09-909-207-4

ALIGNMENTS

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FEATURE
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         RESULT 2
US-09-909-207-5
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; Pred. No. 2.1e-208;
0; Mismatches 0;
  4121-40
                                                                                                                                                                   STRAIN: Bacillus
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SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-909-207-4
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REFERENCE/DOCKET NUMBER: 41:
TELECOMMUNICATION INFORMATION:
TELEFROME: 202-429-0625
TELEFROM: (202) 29-1850
TELEFA: 650 383-5605
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                        744; Conservative
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Best Local Similarity
Matches 744; Conserv
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Xylanase, microorganisms produced it, DNA molecule, processes for preparation of this xylanase and uses thereof
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 744; DB 9; I
100.0%; Pred. No. 2.1e-208;
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APPLICATION NUMBER: 08/470,953
FILING DATE: 06-70ME-1995
ATTORNEY/AGENT INFOMMENTON:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORWATION:
TELEPHONE: 202-429-0625
TELEFAX: (502) 293-1850
TELEFAX: (503) 293-1850
TELEFAX: (503) 293-1850
TELEFAX: (503) 293-1850
TELEX: 650 303-5605
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTELETICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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APPLICATION NUMBER: US/09/909,207
FILING DATE: 19-011-2001
CLASSIFICATION: <Unknown>
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LOCATION: 1..81
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                TITLE OF INVENTION: Xylanase,
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MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
Sequence 5, Application US/09909207
Patent No. US20020115181A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 82..744
                                                                                               ERIC DE BUYL
PIERRE LEDOUX
RENE DETROZ
                                                                         APPLICANT: ANDREE LAHAYE
                                                                                                                                                                                                                                                                                                                               CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN: Bacillus
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Matches 744; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
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FILING DATE: 19-Jul-2001 CLASSIFICATION: «Unknown» PRIOR PAPPLICATION DATE: APPLICATION NUMBER: 08/470,953 FILING DATE: 06-JUNE-1995 ATTORNEY AGENT INFORMATION: REGISTRATION NUMBER: 37,136 REGISTRATION NUMBER: 37,136 FILERPRENEWE ADOCKET NUMBER: 4121:40 TELEPROMUNICATION NUMBER: 4121:40 TELEPROMUNICATION NUMBER: 4121:40 TELEPROMUNICATION NUMBER: 4121:40 TELEPROMUNICATION NUMBER: 4121:40 TELEPROMUNICATION NUMBER: 4121:40 TELEPROMUNICATION NUMBER: 4121:40 TELEPROMUNICATION NUMBER: 4121:40 TELEPROMUNICATION NUMBER: 4121:40 TELEPROMUNICATION NUMBER: 4121:40 TELEPROMUNICATION NUMBER: 4121:40 TELEPROMUNICATION NUMBER: 4121:40 TELEPROMUNICATION NUMBER: 4121:40 TELEPROMUNICATION NUMBER: 4121:40 TELEPROMUNICATION NUMBER: 4121:40 TELEPROMUNICATION NUMBER: 4121:40 TOPOLOGY: 1 linear MOLECULE TYPE: DNA (Genomic) ORIGINAL SOURCE: SEQUENCE DESCRIPTION: SEQ ID NO: 10: US-09-909-207-10	Query Match 100.0%; Score 744; DB 9; Length 1513; Best Local Similarity 100:0%; Pred. No. 3e-208; Actober 744; Oservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 ATGAGACAAAAGAAATTGACGTTGATTTTAGCTTTTTAGTTTTTGCACTAACCTTA 60 Db 620 ATGAGACAAAAGAAATTGACGTTGATTTTTAGTTTTTGCACTAACCTTA 679 Qy 61 CCTGCAGAAATAATTCAGGCACAAATCGTCACCGACAATTCCATTGGCAACCACGATGGC 120 Db 680 CCTGCAGAAATAATTCAGGCACAAATCGTCACCGACAATTCCATTGGCAACCACGATGGC 739	QY 121 TATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGGACAATGATTCTCAATCATTCTCAATCATTGCCTGGACAATGATTTTGGAAAGATAGCGTGGCTCTGGGACAATGATTCTCAATCATGATGCTTGGAAAGATAGAT	
09 121 TATGATTATGAAATTTGGAAAGATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGC 180 121 TATGATTATGAAATTTTGGAAAGATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGATGTTGTGTGTG	0y 481 TCCATTAAGGGATTGCCACATTTAAACAATATTGGAGTGTTTCGAAGATCGAACGCACG 540 Db 481 TCCATTAAGGGATTGCCACATTTAAACAATATTGGAGTGTTCGAAGATCGAACCACG 540 Oy 541 AGTGGCACGATTCTGTCAGCACCACTTTAGAGCGTGGGAAAACTTAGGGATGAATATG 600 Db 541 AGTGGCACGATTTCTGTCAGCACCACTTTAGAGCGTGGGAAAACTTAGGGATGAATATG 600 Oy 601 GGGAAAATGTATGAACCACCATTTTGTGAGAGGCTATCAAAGTAGCGGAAGTGCTAAT 60 Db 601 GGGAAAATGTATGAAGTCGCGCTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAAT 60 Db 601 GGGAAAATGTATGAAGTCGCGCTTACTGTAGAAGGCTATCCAAAGTAGCGGAAGTGCTAAT 60	661 GTATATAGCAATA	Sequence 10, Application US/09909207 Patent No. US20020115181A1 GENERAL INFORMATION: BRIC DE BUYL PIERRE LEDOUX RENE DETROZ TITLE OF INVENTION: Xylanase, microorganisms produced it, PITLE OF INVENTION: Xylanase, microorganisms produced it, NUMBER OF SEQUENCES: 29 CORRESPONDENCE ADDRESS: 29 CORRESPONDENCE ADDRESSEB: WILLIAN BRINKS HOFER GILSON & LIONE STREET: 2000 K St., N.W., Suite 200 CITY: Washington STATE: D.C COUNTRY: U.S.A. ZIP: 20006 COMPUTER READBALE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/909,207

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TITLE OF INVENTION: Xylanase, microorganisms produced it,

PIRENE LEDOUX

FIRENE LEDOUX

TITLE OF INVENTION: Xylanase, microorganisms produced it,

DNA molecule, processes for preparation of this xylanase and uses thereof
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CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
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US-09-909-207-1
; Sequence 1, Application US/09909207
; Patent No. US20020115181A1
; GENERAL INFORMATION:
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DNA molecule, processes for preparation of this xylanase
and uses thereof
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GTATATAGCAATACACTAAGAATTAACGGTAACCCTCTCTCAACTATTAGTAATGACGAG 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/909,207
FILING DATE: 19-Jul-2001
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE
STREET: 2000 K.St., N.W., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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100.0%; Score 744; DB 9;
Best Local Similarity 100.0%; Pred. No. 3e-208;
Matches 744; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR_LINEARY COLDENSING
PRIOR_LING DATA:
APPLICATION NUMBER: 08/470,953
FILING DATE: 06-4010E-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano. Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:
TELEPRONE: 202-49-6625
TELEPRONE: 202-49-6625
TELERAK: (202) 293-1850
TELERAK: (202) 293-1850
TELERAK: GFO 383-5605
INFORMATION FOR SEQ ID NO: 11:
SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION O
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SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-909-207-11
                                                                                                                       721 AGCATAACTTTGGATAAAAAAT 744
                                                                                                                                                                                                                                                           Sequence 11, Application US/09909207
Patent No. US20020115181A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1513 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: mat_peptide
LOCATION: 701..1363
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620..700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN: Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
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US-09-909-207-11
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ERIC DE BUYL
PIERRE LEDOUX
RENE DETROZ
TITLE OF INVENTION: XyJanase, microorganisms produced it,
DNA molecule, processes for preparation of this xylanase and uses thereof
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                                                                                                        682 ATTAACGGTAACCCTCTCTCAACTATTAGTAATGACGAGGCATAACTTTGGATAAAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPPY disk
COMPUTER: IN PC compatible
COMPUTER: IN PC compatible
CORPUTER: IN PC compatible
CORPUTER: IN PC compatible
CORPUTER: IN PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/909,207
FILING DATE: 19-Jul.-2001
CLASSIFCATION: «Unknown>
PRIOR APPLICATION TOWNS
FILING DATE: 06-JUNE-1995
ATTORNEY ARGISTANTION:
NAWE: Wilhlem P: Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REGISTRATION NUMBER: 37,136
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOPER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1..663
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                       ; Sequence 2, Application US/09909207
; Patent No. US20020115181A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5665
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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LOCATION: 1..663
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LENGTH: 663 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ANDREE LAHAYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 29
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STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN: Bacillus
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Best Local Similarity
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               COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: THEN PC Compatible
COMPUTER: THEN PC COMPS. MS. DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/909,207
FILING DATE: 19-Jul-2001
CLASSIFICATION NUMBER: US/04/0,953
FILING DATE: 06-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELEPHONE: 202-429-0625
TELEPHONE: 202-429-0625
TELEPAX: (5202) 293-1850
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 663;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN: Bacillus
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 663 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
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                               CAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAA
                                                           1 CAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGGAAT
                                                                                         GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGG
                                                                                                                                                     AACAATGTTAACAACATATTATTCCGTAAAGGTAAAAAATTCAATGAAACACAAACACAC
                                                                                                                                                                                                              CAACAAGTTGGTAACATGTCCATAAACTACGGAGCCAACTTCCAAACCAAATGGTAATGCG
                                                                                                                                                                                                                                          TATTTATGCGTCTATGGTTGGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGT
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                                                                                                                                                                                                                                                                                                                                                       TGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTTGATGGAGGA
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Patent No. US20010024815A1

GENERAL INFORMATION:

APPLICANT: M ntyl, Arja

APPLICANT: Pagerstr m, Richard

APPLICANT: Lantro, Raija

APPLICANT: Lantro, Raija

APPLICANT: Suominen, Pirkko

APPLICANT: Suominen, Pirkko

APPLICANT: Lahtinen, Tarja

TITLE OF INVENTION: Production and Secretion of Proteins of

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
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0; Mismatches
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 663; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MNS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: 08/590,563
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nucleic acid
EDNESS: No. US20010024815A1 Relevant
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PRIOR PAPPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-UUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BUGAISTRY LAWFENCE B.
REGISTRATION NUMBER: 35,086
REGISTRATION NUMBER: 35,086
REGISTRATION NUMBER: 35,086
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2600
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TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2600
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
CONTRACTOR SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 57.13
Matches 238; Conservative
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US-09-770-621-1
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NAME/KEY:
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                                                              APPLICANT: Mantyla, Arja
APPLICANT: Mantyla, Arja
APPLICANT: Daloteimo, Marja
APPLICANT: Lantto, Raija
APPLICANT: Lahtinen, Tarja
APPLICANT: Lohtinen, Tarja
APPLICANT: Suominen, Pirko
APPLICANT: Suominen, Pirko
APPLICANT: Vehmaanpera, Jari
TITLE OF INVENTION: Production and Secretion of Proteins in Filamentous
TITLE OF INVENTION: Pungi
TITLE OF INVENTION: Pungi
TITLE OF INVENTION: Pungi
TITLE OF INVENTION: Pungi
TITLE OF INVENTION: Pungi
FILE REFERENCE: 1716, 0340004
CURRENT FILING DATE: 1098-07-23
PRIOR PILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-24
PRIOR FILING DATE: 1999-01-24
PRIOR FILING DATE: 1996-01-26
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Version 3.0
SEQ ID NOS: 18
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16.0%; Score 119.4; DB 15; Length 1375;
Best Local Similarity 57.1%; Pred. No. 3.1e-24;
Matches 238; Conservative 0; Mismatches 176; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Actinomadura flexuosa (Strain: DSM43186)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (303)...(1337)
OTHER INFORMATION: Product= AM35 xylanase
Sequence 1, Application US/10286993
Publication No. US20030148453A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1375
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Sequence 39, Application US/10307441 Publication No. US20030166236A1 GENERAL INFORMATION:
APPLICANT: SUNG, Wing L.

US-10-307-441-39

Sequence 71, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
 APPLICANT: Jiang, Bo
 APPLICANT: Storms, Reg
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: BNZYMES AND METHODS OF USE
; FILE REFERENCE: 1018-0999
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71 APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
TITLE OF INVENTION: and Alkalophilicity
TITLE OF INVENTION: and Alkalophilicity
CURRENT G27367-5006US
CURRENT PLICATION NUMBER: US/10/307,441
CURRENT PLICATION NUMBER: PCT/CA01/00769
PRIOR PRICATION NUMBER: PCT/CA01/00769
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PARCHAIN Ver. 2.1
SEQ ID NO 39
LENGTH: 596 191 AATAAGGTGATCAACTTCTCGGATCTTATAATCCGAATGGGAATTCATACTTAAGCGTC 250 311 AATCCGAGTACCGGCGCCACAAATTAGGCGAAGTCACTAGTGATGGATCCGTATATGAT 370 510 371 ATCTACCGTACCCAACGCGTTAATCAGCCATCGATCATTGGAACCGCCACCTTTTATCAG 430 490 AGAGCGTGGGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCGCTTACTGTA 630 251 TATGGCTGGTCTAGAAGCCACTGATTGAATATTACATTGTCGAAAATTTCGGTACCTAC 310 ATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATTTAAACAA 431 racriegaererracionarcarceses de controcorrador de contra de co 491 AATGCATGGCACAGCCAAGGGTTAACCCTAGGTACAATGCATTATCAAATCGTAGCGTG TATTGGAGTGTTCGAAGATCGAAGACGCACGAGGCACGATTTCTGTCAGCAACCACTTT 394 CGTCC---ACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGAACATATGAT 274 AACATGTCCATAAACTACGGAGCCAACTTCCAACCAAATGGTAATGCGTATTTATGCGTC Gaps ë, Query Match 15.5%; Score 115.2; DB 15; Length 596; Best Local Similarity 57.7%; Pred. No. 3.5e-23; Matches 226; Conservative 0; Mismatches 163; Indels 3; ; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: TrX US-10-307-441-39 ORGANISM: Aspergillus LENGTH: 942

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RESULT 12
US-10-213-990-68
; Sequence 68, Application US/10213990
; Sequence 68, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Storms, Reg
APPLICANT: Roemer, Reg
APPLICANT: Roemer, Reg
TITLE OF INVENTION: WICLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
TITLE OF INVENTION: BUZYWES AND METHODS OF USE
FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 705
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Pred. No. 3e-21;
0; Mismatches 267;
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Best Local Similarity 51.9%;
Matches 298; Conservative
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FEATURE:
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; LOCATION: (1)...(705)
US-10-213-990-68
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Publication No. US20030082595A1
GENERAL INFORMATION.
GENERAL INFORMATION.
GENERAL INFORMATION.
GENERAL INFORMATION.
APPLICANT: Bussey, Howard
APPLICANT: Bussey, Howard
APPLICANT: Roemer, Terry
TITLE OF INVENTION: BYZYMES AND METHODS OF USE
FILE REFERENCE: 10182-019-99
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                        0; Mismatches 166; Indels
                                                                                                                                                                                                                               DB 14;
                                                                                                                                                                                                                           Score 111.4; DB 1
Pred. No. 5.9e-22;
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57.0%;
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llarity 57.8%;
Conservative
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Matches 224; Conservative
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; ORGANISM: Aspergillus
US-10-213-990-70
                                               ) NAME/KEY: CDS
; LOCATION: (1)...(942)
US-10-213-990-71
                                                                                                                                                                                                                                                                 Similarity
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US-10-213-990-70
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Best Local S:
Matches 216
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Sequence 64, Application US/10213990
| Sequence 64, Application US/10213990
| Publication No. US20030082595A1
| GENERAL INCORMATION:
| APPLICANT: Jiang, Bo
| APPLICANT: Storms, Reg
| APPLICANT: Storms, Reg
| APPLICANT: Roemer, TCLETC
| TITLE OF INVENTION: BUZYMES AND METHODS OF USE
| TITLE OF INVENTION: BUZYMES AND METHODS OF USE
| TITLE OF INVENTION: USCA.012-019-99
| CURRENT APPLICATION NUMBER: US/10/213,990
| CURRENT FILING DATE: 2002-08-05
| NUMBER OF SEQ ID NOS: 72
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 64
| LENGTH: 712
                                                                                                                                                                                                                                                                                                                                     1940 AGCATGCAAGCCACTTGGACTTGAAATGGGCACTTATAACTATATGATTGTGTCCCCGA 1999
                                                                                                                                                                                 330 CGICIAIGGIIGGACIGIIGACCCICIIGICGAATAITAITAITIGICGACAGTIGGGGCAA 389
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                                       CTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGGATTGCCACATTTAAACAATA
                                                                                                                                         TTGGAGTGTTCGAAGGATCGAAGGCACGAGTGGCACGATTTCTGTCAGCAACCACTTTAG
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Pred. No. 4.5e-20;
0; Mismatches 172; Indels
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al Similarity 55.8%;
221; Conservative
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; ORGANISM: Aspergillus
US-10-213-990-64
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Best Local Similarity
Matches 221; Conserv
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US-10-213-990-64
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                     ATATGATATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGGATTGCCACATT
                                                         474 TTACAACATCTACAGGCCGTTCGCTACAATGCTCCCTCCATCGAAGGCACCAAGACCTT
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TITLE OF INVENTION: PENTILLIUM FUNICULOSUM STRAIN USEFUL
TITLE OF INVENTION: PENTILLIUM FUNICULOSUM STRAIN USEFUL
TITLE OF INVENTION: PENTILLIUM FUNICULOSUM STRAIN USEFUL
TITLE OF INVENTION: PENTILLIUM FUNICULOSUM STRAIN USEFUL
CURRENT APPLICATION NUMBER: US/10/299,393
CURRENT APPLICATION NUMBER: US/462,246
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 14
SOFFWARE: FRAESEQ for Windows Version 4.0
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Pred. No. 4.1e-20;
0; Mismatches 165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       624 TACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCT
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Publication No. US20030108642A1
GENERAL INFORMATION:
APPLICANT: Sabatier, Alain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Penicillium funiculosum
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Best Local Similarity 56.5%;
Matches 218; Conservative
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LOCATION: (1317)...(1589)
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LOCATION: (1590)...(1642)
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LOCATION: (570)...(576)
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LENGTH: 2898
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US-10-299-393-1
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US-10-213-990-65

Sequence 65, Application US/10213990

Publication No. US20030082595A1

GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Storms, Reg

APPLICANT: Roemer, Terry

TITLE OF INVENTION: BUZYMES AND METHODS OF USE

TITLE OF INVENTION: BUZYMES AND METHODS OF USE

TITLE OF INVENTION: BUZYMES AND METHODS OF USE

CURRENT APPLICATION NUMBER: US/10/213,990

CURRENT APPLICATION NUMBER: US/10/213,990

CURRENT FILING DATE: 2002-08-05

NUMBER OF SEQ ID NOS: 72

SOFTWARE: PRACEED FACED OF WINDOWS VERSION 4.0

SEQ ID NO 65

LENGTH: 666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           403 --GGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGAACATATGATATCTACGAGA 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     392 CGGGAGCCACCCATCTCGGCACCGTCGAGGGGGCCACGTACAACCTCTACAAGA 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGACGCGGACGATGCGCCGTCCATCCAGGCACGGCTACTTTTGACCAGTACTGGTCG 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 14; Length 666;
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Job time : 476.684 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 56.3
Matches 215; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Aspergillus
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NAME/KEY: CDS

LOCATION: (1)...(666)

US-10-213-990-65
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BM134812 CR008236 CR055280 CR895680 BQ166480 CC820765 AJ63794 CC033374 CD033274 CD033274 CD033274 CM278095 BM1375180 CM278095 BM1375180 CMS007JU

AJ637947

Drosophil BJ401024

BJ398920

BJ372089 BJ402691

> BJ372089 BH066221 BJ398920

WHE2624 C

WHE0821-0 WHE0452 F WHE2638 H

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/db xrefe"taxon: 1352"
/clone="RTDS1_9 C03_A015"
/lab host="BTDS1_9 C03_A015"
/lab host="BH10B-T1 phage-resistant E. coli"
/clone lib="brought-stressed loblolly pine roots DS1"
/note="Vector: pS11180; Site 1: EcoR1; Site 2: Xho1; The
library was prepared from polyA+ RNA from drought-stressed
loblolly pine (Pinus taeda) roots. Water was withheld from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mmprattenga.edu

RNA prepared and library constructed by W. Walter Lorenz, School of

Foreerry, University of Georgia; plant material prepared at the

Foreerry, Florida; sequencing done in the Laboratory for

Genomics and Bioinformatics, University of Georgia. Sequence ends

have been trimmed to exclude vector and regions below Phred quality

16. Three-prime sequences are presented as their reverse complement

and have been trimmed to exclude polyA.

Seq primer: JENREY (CAGGAAACAGCTATGACC).
                                                                                                                                                                                                                                                                                                                              RIDSI 9 C03.91 A015 Drought-stressed loblolly pine roots DSI Finus
                                                                                                                                                                                                                                                                                                                                                                                                              Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. (bases 1 to 618)
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An EST database from drought-stressed loblolly pine (Pinus taeda)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J., Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Other_ESTB: RIDS1 9 C03.bl A015
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Pinus taeda"
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Pinus taeda
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/strain="CCLONES"
                                                                                                                                                                                                                                                                                                                                                                   CF472462.1 GI:34489834
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roots
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                                                                            November 10, 2004, 16:24:32 ; Search time 3225.17 Seconds (without alignments) 8406.125 Million cell updates/sec
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CN132941
CCN132941
CCN89803 C
CE89803 C
CD464145 E
CD46813 N
AQ160513 N
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CD458837
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
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An EST database from Sorghum: oxidatively stressed leaves and roots Unpublished (2003)

Other ESTS: OXI,9 D10.91 A002

Coher ESTS: OXI,9 D10.91 A002

Faboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Sorghum.
                                                                                                                                  ECORI
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ramet clones until predawn needle water potential re-1.75 MPa. On day 7 roots were harvested for RNA isolation. Double-etranded cDNA was cloned unidirectionally into p511180. Inserts excised with (5' end) and XhoI (3' end)."
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Seg primer: Sug3-14 (TAGTCTAGCGGCCGCACC)
POLYA=Yes.
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Sorghum bicolor
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/db xref="taxon:4558"
/clone="0X19 D10 A002"
/lab host="mild=Tri phage-resistant E. coli"
/lab host="mild=Tri phage-resistant E. coli"
/clone lib="Oxidatively-stressed leaves and roots"
/clone lib="Oxidatively-stressed leaves and roots"
/note="Organ: Leaf and Root; Vector: pME188-FL3; Site_1:
Xhoi; Site_2: Xhoi; The library was prepared from polyA+RNA from oxidatively stressed, hydroponically grown sorghum seedlings. At 8 days of age, growth medium was supplemented with hydrogen peroxide to 0.003% and leaves were misted with 10 um methyl viologen. Leaves and roots were harvested at 3, 12 and 27 hr after treatment and all tissue pooled. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME188-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACTGTGTG, insert."
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Best Local Similarity 53.9%; Pred. No. 3.9e-15;
Matches 214; Conservative 0; Mismatches 180;
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organism="Sorghum bicolor"
                                                         /mol_type="mRNA"
/cultivar="BTx623"
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linear EST 31-OCT-2003
Version 6 October 2003
mRNA sequence.
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/clone_lib="T.reesei mycelial culture, Version 6 October
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Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaces; Hypocrea.
1 (bases 1 to 744)
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                                                                                                                                                                                                                                                                                                                                             Hypocrea jecorina (anamorph: Trichoderma reesei)
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55.0%; Pred. No. 8.5e-15;
tive 0; Mismatches 162;
                                                                      744 bp mRNA tricol3xe09.bl T.reesei mycelial culture, Hypocrea jecorina cDNA clone tricol3xe09, CP867983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
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clone="tric013xe09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 919-513-0024
Email: ralph dean@ncsu.edu
Seg primer: LT-Fl primer.
Location/Qualifiers
                                                                                                                                                                                                                                                         CF867983.1 GI:38122635
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Best Local Similarity 55.0°
Matches 202, Conservative
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                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
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RESULT 4
CF867983
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/db xref="taxon.458"
/clone="0X1_9_D10_A002"
/lab host="DH10B-T1 phage-resistant E. coli"
/clone 11="Oxidatively-stressed leaves and roots"
/clone 11="Oxidatively-stressed leaves and roots"
/clone 11="Oxidatively-stressed leaves and roots"
/note="Organ: Laef and Root; Vector: pME18S-FL3; Site_1:
XhoI; Site_2: XhoI; The library was prepared from polyA+
RNA from oxidatively stressed, hydroponically grown
sorghum seedlings. At 8 days of age, growth medium was
supplemented with hydrogen peroxide to 0.003% and leaves
were misted with 10 um methyl viologen. Leaves and roots
were harvested at 3, 12 and 27 hr after treatment and all
tissue pooled. Double-stranded cDNA was cloned
unidirectionally into different DralII sites of the
pME18S-FL3 vector. (5-prime DralII site is CACTGTGTG,
3-prime DralII site is CACCATGTG). XhoI excises the cDNA
                                                                                                                                                                                                                                                                                                             Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Bhred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
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                                                                               Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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Location/Qualifiers
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/mol_type="mRNA"
/cultivar="BTx623"
    ESTS: OX1 9 D10.b1 A002
                                                                                                                                                                                                                             Tel: 706 542 1860
Fax: 706 583 0210
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                                                                                                         768 GGAGGGT
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                               631
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Best Local
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ORGANISM
                                                                                                                                                                                                                                                                                                 LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                   RESULT 6
CD464145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 AACATGTCCATAAACTACGGAGCCAACTTCCAACCAAATGGTAATGCGTATTTATGCGTC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   408 AACAAGSTCATCAACTTCTCGGGCAGCTACAACCCCAACGGCAACACTTCTCCGTG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 CGTCCACCA---GGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGAACATATGAT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACGGCTGGTCCCGCAACCCCCTGATCGAGTACTACATCGTCGAGAACTTTGGCACCTAC 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            708 AACGCGTGGGCTCAGCAAGGCCTGACGCTCGGGACGATGGATTACCAGATTGTTGCCGTG 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="tricollaxe09"
/dev stage="mycelia"
/clone lib="T.recelia" mycelial culture, Version 3 april"
/note="Vector: pREP3Y; Site_1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."
                                                                                                                                                                            CB898036 1.reesei mycelial culture, Version 3 april Hypocrea
jecorina cDNA clone tric013xe09, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   451 ATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGAATTGCCACATTTAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypocreomycetidae, Hypocreales, Hypocreaceae, Hypocrea.

1 (bases 1 to 799)

Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S., Dunn-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G.J., Kelley, A.S., Meerman, H.J., Mitchinson, C., Olivares, H.A., Teunissen, P.J., Yao, J. and Ward, M. Tengulation of biomass-degrading enzymes in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACCCGTCCACGGGCGCCACCAAGCTGGGCGAGGTCACCTCCGACGGCAGGGTCTACGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
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Pred. No. 8.7e-15;
0; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'organism="Hypocrea jecorina"
|mol_type="mRNA"
|strain="QM6a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:51453"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genencor Intl.
925 page Mill Road, Palo Alto,
Tel: (650) 846-7635
Fax: (650) 621-7817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: Pforeman@genencor.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seg primer: LT-Fl primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Pamela K. Foreman
                                                                                                                                                                                                                                                                                                                                     CB898036.1 GI:30112694
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55.0%;
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Best Local Similarity
GGAGGGT
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                                                                                                                                                                                                                       DEFINITION
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PUBMED
                                                                                                             RESULT 5
CB898036
                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
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/mol_type="mRNA"
/cultivar="BTx623"
/db_tref="BTx623"
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/clone lib="Ethylene-treated seedlings"
/clone lib="Ethylene-treated seedlings"
/clone lib="Ethylene-treated seedlings"
/clone lib="Ethylene-treated seedlings"
/clone lib="Ethylene-treated from polyA+ RNA from seedlings grown
in hydroponic culture. At 8 days of age, medium was
supplemented with 0.5 mM 1-aminocyclopropane-1-carboxylic
acid (ACC) to induce endogenous ethylene (ETH) production.
Roots and shoots were harvested after 27 and 72 hr and
                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Sorghum.

(Dasse 1 to 738)

Cordonnier-Pratt, M.-M., Wentzel, V., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Shah, M., Salzman, R., Olua Tan, N., Gonzalez, M., Lane, S., Miller, V., Nanda, P., An Est database from Sorghum: 1-aminocyclopropane-1-carboxylic acid
CD464145
ETH1 48 B06.gl A002 Ethylene-treated seedlings Sorghum bicolor CDNA clone FTH1_48_B06_A002 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & Winiversity;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACCATGTG). XhoI excises the CDNA insert."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 CCATAAACTACGGAGCCAACTTCCAACCAAATGGTAATGCGTATTTATGCGTCTATGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ACC)-treated seedlings
Unpublished (2003)
Other ESTS: ETH1 48 B06.b1 A002
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
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53.5%; Pred. No. 2.6e-13;
trive 0; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: Sug5 (CTTCTGCTCTAAAAGCTGCG)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Sorghum bicolor"
                                                                                                                                                                                                                                                      Sorghum bicolor (sorghum)
Sorghum bicolor
                                                                                                                                                                         CD464145.1 GI:31385413
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Gaps

3,

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401 465

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/tissue_type="Protoplasts"
/lab_hogt="E. coli DH10B"
/clone lib="CuGI Rice Blast BAC Library"
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devestating fungal diseases
of rice world wide. It is a filamentous ascomycete with
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V.Y., Zhul., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M. Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                341 GGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGTTGGGGCAACTGGCGTCCAC
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Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Pred. No. 2.2e-12;
0; Mismatches 186; Indels
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/mol_type="genomic DNA"
/strain="70-15"
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Clemson University Genomics Institute
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/clone="mgxb0006C21r"
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Class: BAC ends
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                                                       GGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGTTGGGGCAACTGGCGTCCAC 400
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Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
1 (bases 1 to 921)
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A CDNA library prepared from Fusarium graminearum grown on a complex plant subserrate Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Watson, Robert.J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 20, Central Experimental Farm, Ottawa, Ontario, KlA
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/organism="Gibberella zeae"
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/lab_host="E. coli DH10B"
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/strain="DAOM 180378"
/db_xref="taxon:5518"
/clone="F908_04b10"
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Fax: (613) 759-1701
Email: watsonrj@agr.gc.ca.
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unploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25% genome coverage. High density colony filters are available upon request."
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Phillips,K., Sasinowski,M. Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
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Pred. No. 2.9e-12;
0; Mismatches 197; Indels
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Magnaporthe_grisea
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson Universiy, Clemson, SC:
Tel: 864 656 4537
Fax: 864 656 459
Email: rdean@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
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                                                                                                                                                                                                                                                                                                                DRIGIN
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/lab host="E. coli DH10B"
/lab host="E. coli DH10B"
/clone lib="CUGI Rice Blast BAC Library"
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal host interaction. In order to facilitate genome wide analysis, a BAC library contentining 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."
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Magnaporthe grisea
Magnaporthe grisea
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetes incertae sedis, Magnaporthaceae, Magnaporthe.
1 (bases 1 to 720)
Yu. Y., Zhu.H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M, Wing, R.A. and Dean, R.A.
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0; Mismatches 168; Indels
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                                                                                                                                                grisea"
                                                                                                                                                                                                                                                                                                               /tissue_type="Protoplasts"
                                                                                                                                         organism="Magnaporthe"
                                                                                                                                                                                                                                            /db_xref="taxon:148305"
/clone="mgxb0005C20f"
Class: BAC ends
High quality sequence stop: 263.
Location/Qualifiers
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Best Local Simi
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AQ160254 1750 bp DNA linear GSS 09-SEP-1998 agxb00031,19r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
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N.Y., Zhul,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
Philips,K., Sasinowski,M. Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
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Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 655 5737
Fax: 864 656 4293
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// note="Wetcor: pBACWICH; Site_1: HindIII; Site_2: HindIII;
// note="Wetcor: pBACWICH; Site_1: HindIII; Rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average innext size of 130 kbp was constructed. This library represents greater
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                                                                                                                                                                      Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 655 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
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11.0%; Score 82.2; DB 8;
Best Local Similarity 54.1%; Pred. No. 4.5e-12;
Matches 236; Conservative 0; Mismatches 189;
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Class: BAC ends
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Location/Qualifiers
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                               526 AGATCGAAACGCACGAGTGGCACGATTTCTGTCAGCAACCACTTTAGAGCGTGGGAAAAC 585
                                                                                                   586 TTAGGGATGAATATGGGGAAAATGTATGAAGTCGCG---CTTACTGTAGAAGGCTATCAA 642
210 CGCTACAACCAGCCCTCCATCGACGGCACCAAGACCTTTCAGCAGTTCTGGTCGGTGCGC 151
                                                                                                                        90 GCCGGCCTCAACCTCGGCAACCAGTGGAACTACCAGATCCTGGCCGTCGAGGGCTACCAC 31
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1. (bases 1 to 786)

1. (v. x, Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Sasinowski, M. Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                 150 CGCAACAAGCGCCCAGCGGCACCGTCACCTTTGCCAACCACGTCAACGCCTGGCGAAC
                                                                                                                                                                                                                                                                                                                                                                                                         Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 5737
Fax: 864 665 6737
Email: rdean@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                         Magnaporthe grisea (anamorph: Pyricularia grisea)
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mol_type="genomic DNA"
strain="70-15"
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Seg primer: GGAAACAGCTATGACCATG
Class: BAC ends
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High quality sequence stop: 468.
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229 AAAGGTAAAAAATTCAATGAAACACAAAAACACCAACAAGTTGGTAACATGTCCATAAAC 288

11.0%; Score 81.6; DB 8; Length 786; llarity 54.1%; Pred. No. 6.8e-12; Conservative 0; Mismatches 189; Indels 11;

Query Match Best Local Similarity Matches 236; Conserva

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mgxb0001B24f CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0001B24f, genomic survey sequence.
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500 AAAGGAAAAAAAGAGACTAACAACAACAACAACAAAAA.----CAGCCGCGTCATCAAC 446
                                                                                                289 TACGGAGCCAACTTCCAACCAAATGGTAATGCGTATTTATGCGTCTATGGACTGTT 348
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1 (bases 1 to 583)

Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Saainowski, M. Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 655 5737
Fax: 864 656 4293
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/strain="70-15"
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Seg primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 411.
Location/Qualifiers
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561 bp DNA linear GSS 06-MAR-1999 mgxb0010M14£ CUGI Rice Blast BAC Library Magnaporthe grisea genomic AQ396475
blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25% genome coverage. High density colony filters are available upon request."
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes; Sordariomycetes; Magnaporthe.
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100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Exar: 864 656 4293
Email: rdean@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
Class: BAC manity sequence start: 50
High quality sequence stop: 443.
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Clemson University Genomics Institute
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Eukaryotta.

Eukaryotta.

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Eukaryotta.

Eungi, Ascomycotta.

Eungi, Ascomycotta.

Mycosphaerella.

I (Dases 1 to 617)

Keon, J. P. R., Hargreaves, J. A., Antoniw, J. F. and Hammond-Kosack, K.

Analyais of expressed sequence tags from the wheat fungal leaf

blotch pathogen, Mycosphaerella graminicola (anamorph Septoria

tritici)
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53.7%; Pred. No. 1.7e-10;
iive 0; Mismatches 170;
'organism="Magnaporthe grisea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              are available upon request."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fungal Genet. Biol. (2004) In press
                                                                   /mol_type="genomic DNA"
/strain="70-15"
                                                                                                                                                                                                                  xref="taxon:148305"
                                                                                                                                                                                                                                                                                                     /clone="mgxb0010M14f"
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Matches 204; Conservative
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/db xref="taxon:54734"
/clone="mgcl2d03f"
/clone=lib="MgC"
/clone lib="MgC"
/note="vector: pSPORT1; Library constructed from senescent wheat leaves 21-25 days after infection with Mycosphaerella graminicola exhibiting abundant hyphal growth and asexual sporulation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 CCATAAACTACGGAGCCAACTICCAACCAAATGGTAATGCGTATTTATGCGTCTATGGTT 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               458 AGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATTTAAACAATATTGGA 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 55.6%; Pred. No. 1.9e-10;
Matches 168; Conservative 0; Mismatches 131; Indels

    617
    ^617
    ^6xgania="Mycosphaerella graminicola"
    ^mol_type="mRNA"
    ^etrain="Strit"

                                                                Former Herts, UNITED KINGDOM Tel: +44(0)1582 763133
Fax: +44(0)1582 763981
Email: john.keon@bbsrc.ac.uk
Insert Length: 800 Std Error: 100.00
Seg primer: M13 reverse.
Location/Qualifiers
Contact: Keon J
Plant Pathogen Interactions Division,
Rothamsted Research,
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of preparation and use thereof
Patent: EP 0698667-A 10 28-FEB-1996;
SOLVAY (BE)
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            AB029319 Bacillus X59059 Bacillus sp A42251 Sequence 1 A42285 Sequence 35 AR127019 Sequence AR220023 Sequence AR221306 Sequence AR221306 Sequence AR221306 Sequence AR221306 Sequence AR221306 Sequence AR220095 Bacillus AF90981 Bacillus AF220052 Bacillus AF220052 Bacillus AF220052 Bacillus AF220052 Bacillus AF220052 Bacillus AF220050 Sequence 30 AR127045 Sequence AR27045 Sequence AR220050 Sequence
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AR17325 Sequence 1
AR8223 Sequence 1
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AR193050 Sequence 2
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A48232 Sequence 11
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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/brotein_id="CAA0194.1"
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1 (Dases 1 to 1513)
De, B.E., Lahaye, A., Ledoux, P. and Detroz, R.
Xylanase, microorganisms for its production, DNP
of preparation and use thereof
Patent: EP 0698667-A 11 28-FEB-1996;
SOLVAX (BE)
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100.0%; Pred. No. 1.5e-295;
ive 0; Mismatches 0;
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Other publication BE 1008750 960604
Other publication BR 9503454 960305
Other publication FI 953578 960127
Other publication FI 953578 960127
Other publication AV 2508695 960208
Location/Qualifiers
1. 1513
/organism="unidentified"
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/db_xref="taxon:32644"
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Sequence 11 from Patent EP0698667.
A48232.
A48232.1 GI:2302079
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/note="unnamed protein
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                                                                       ccrigarcecritaaririgiaaacririarririagiriracereargricecrearicarac
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Qy 1381 TTCGGTTCAGTTCTCATTATTTTCAAATAACCTCCGGTTGGATCTTTTCCAACGGGAGG 1440 Db 1381 TTCGGTTCAGTTCTTTTTCAATAACCTCCCGGTTGGATCTTTTCCAACGGGAGG 1440 Qy 1441 TTTATTGGAAAGGTTAAGTATAGTATACTCCGATTCCATCCA	RESULT 4 AR193056 LOCUS LOCUS DEFINITION Sequence 11 from patent US 6346407. ACCESSION AR193056 VERSION AR193056.1 GI:20239021 KEYWORDS SOURCE ONGANISM UNKNOWN.	Unclassified. REFERENCE 1 (bases 1 to 1513) AUTHORS De Buyl,E., Lahaye,A., Ledoux,P. and Detroz,R. AUTHORS De Buyl,E., Lahaye,A., Ledoux,P. and Detroz,R. TITLE Xylanase, microorganisme producing it, DNA molecules, methods for JOURNAL Patent: US 6346407-A 11 12-FEB-2002; FEATURES Location/Qualifiers Source /organism="unknown" /mol_type="unassigned DNA"	Query Match Query Match Best Local Similarity 100.0%; Score 1513; DB 6; Length 1513; Best Local Similarity 100.0%; Pred. No. 1.5e-295; Matches 1513; Conservative 0, Mismatches 0; Indels 0; Gaps 0; Qy 1 AMATTGAATTGTATATCTAATGATAACGACAATGGTCACTGTTTTAAACTAATCTC 60	61 AAACCAATACTTCTTTATTTAACGCTAACCACTGCAATCTTATCACAAGAACATTCTTT 61 AAACCAATACTTCTTTATTTAACGCTAACCACTTGCAATCTTATCACAAGAACATTCTTT 61 AAACCAATACTTCTTTAATTTAAACGCTAACCACTTGCAATCTTTATCACAAGAACATTTTATCTTTTTATCTTTTATCTTTTATCTTTTATCTTTATCTTTATCTTATTA	181 CCTTGATCGGTTTAATTTGTAAACTTTATTTTAGTTTACGTGATGTTCCCTCATTCAT	301 ATTTATGTCATATTTCTCACGCCCTCCATAATGGAATATATAT	421 AGCAGCTATCCAAAAACACTGATGTTGACCTCTTAAAGAGTGTCACTATCTAT
241 CATTAATCACAGTTAACGCTAGAGTCATCTTTTTCGGTTCTCAAAATACCTGAAGAAC 300 301 ATTTATGTCATATTTCTCACGCCGCTCCATAATGGAATATATAT	481 GATAATTATCCAGTTTCAAAATTGAAATAGTGTGTATGGAATAGTTTGAATGTCAACTG 540	601 THANAGGGGALGCCTAILGHANN GOOD GOOD GOOD GOOD GOOD GOOD GOOD GO	781 AATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGGAACAATGTTAACAACATATT 840	901 CATAAACTACGGAGCCAACTTCCAACCAAATGGTAATTATGCGTCTATGGTTG 960	1021 AGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGACATATGATATCTACGAGAC 1080 1021 AGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGACATATGATATCTACGAGAC 1080 1021 AGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGACATATCTACGAGAC 1080 1081 TCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGTGT 1140 1081 TCTTAGAGTCAATCACCCTCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGTGT 1140	1141 TCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGCAACCACTTTAGAGCGTGGGA 1200 1141 TCGAAGATCGAAAACGCACGAGTGGCACGATTTCTGTCAGCAACCACTTTAGAGCGTGGGA 1200 1201 AAACTTAGGGAAAATGGGGAAAATGTATGAAGTCGCGCTTACTGTAGAAGCTTACA 1260 1201 AAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCGCTTACTGTAGAAGCTATCA 1260 1201 AAACTTAGGGATGAATATGGGGGAAAATGTATGAAGTCGCGCTTACTGTAGAAGGCTATCA 1260	1261 AAGTAGCGAAGTGCTAATGCAATACAATAACGAATTAACGGTAACCTCTCTC 1320

1220 GGGAAAATGTATGAAGTCGCGCTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAAT 1279

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   GGTACGTTCAGTGCCCAATGGAACAATGTTAACAACATATTATTCCGTAAAAGGTAAAAAA 240
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De Buyl, E., Lahaye, A., Ledoux, P. and Detroz, R.
Xylanase, microorganisms producing it, DNA molecules, methods for preparing this xylanase and uses of the latter
Patent: US 6346407-A 4 12-FEB-2002;
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                                  TTCAATGAAACACAAAACACACCAACAAGTTGGTAACATGTCCATAAACTACGGAGCCAAC
                                                                  Trcaargaaacacaaacaccaacaacractrccraacarcracarcaraacraccaac
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Pred. No. 3.9e-140;
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/organism="unknown"
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(S De, B.E., Lahaye, A., Ledoux, P. and Detroz, R.

Xylanage, microorganisms for its production, DNA molecules, process of preparation and use thereof.

M. Patent: EP 6698667-A 5 28-FEB-1996;

SOLVAY (BE)

Other publication BE 1008751 960702

Other publication BR 9503454 960305

Other publication FR 9503454 960305

Other publication AU 2508695 960127

Other publication AU 2508695 960127

Other publication AU 2508695 96027
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llarity 100.0%; Pred. No. 3.9e-140;
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'note="unnamed protein product"
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              CCTGCAGAAATAATTCAGGCACAAATCGTCACCGACAATTCCATTGGCAACCACGATGGC
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CCTGCAGAAATAATTCAGGCACAAATCGTCACCGACAATTCCATTGGCAACCACGATGGC
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Dalboege, H., Didericheen, B., Sandal, T. and Kauppinen, S. METHOD OF PROVIDING NOVEL DNA SEQUENCES
Patent: WOY3409-A 1 20-NOV-1997;
NOVONORDISK AS (DK)
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Abaxef="G1:4756811"
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ANVYSNTLRINGNPLSTISNDKSITLDKNN"
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                                                                                                                                                                         47.2%; Score 713.6; DB 6;
.larity 97.4%; Pred. No. 5.4e-134;
Conservative 0; Mismatches 19;
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                                                    Sandal, T., Kauppinen, M. Sakari.
                                1 (bases 1 to 744)
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Diderichsen, Bslashedrge.
Method of providing a hybrid polypeptide exhibiting
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Pred. No. 5.4e-134;
); Mismatches 19;
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97.4%;
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Matches 725;
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RESULT 11

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AR163110 Sequence 1 from patent 1 AR163110 AR163110.1 GI:16233600

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AGTGGCACGATTTCTGTCAGCAACCACTTTAGAGCGTGGGAAAACTTAGGGATGAATATG 1219
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Williams, D.P., Iverson, S., Farrell, R.Lee., Van Solingen, P.,
Harbes, W.Theresia., Van Der Kleij, W.Antonius. H.. Van
Beckhoven, R. Franciscus. C., Quax. W.Johannes., Herwijer, M.Adriana.,
Goedegebuur, F. and Jones, B. Edward.
Alkalitolerant xylanases
Patent: US 6140095-A 18 31-OCT-2000;
Location/Qualifiers
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                                            TCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGTGTTCGAAGATCGAAACGCACG
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44.5%; Score 673.6; DB 6;
Best Local Similarity 95.7%; Pred. No. 6.5e-126;
Matches 714; Conservative 0; Mismatches 29;
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Sequence 18 from patent US
AR117325
AR117325.1 GI:14098231
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/codon etart=1
/codon etart=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22
                                                                                              unidentified
unidentified
unclassified.
1 (bases 1 to 744)
1 (bases 1 to 744)
Van,S.P., Williams,D.P., Iverson,S., Farrell,R.L., Herbes,W.T.,
Van,D.K., Herweijer,M.A., Van,B.R., Quax,W.J., Goedegebuur,P. and
Jones,B.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       920 TTCCAACCAAATGGTAATGCGTATTATGCGTCTATGGTTGGACTGTTGACCCTCTTGTC
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Pred. No. 6.5e-126;
0; Mismatches 29;
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Patent: WO 9518219-A 18 06-JUL-1995;
GIST BROCADES NV (NL)
Other publication JP 8507221T 960806
Other publication BR 940594 951226
Other publication NO 953312 951019
Other publication FI 953920 950831
Other publication AU 1415995 950717.
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/isolate="CBS672.93"
/db_xref="taxon:32644"
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Sequence 18 from Patent WO9518219.
A45313
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1 (Dases 1 to 663)
S De, B.E., Lahaye, A., Ledoux, P. and Detroz, R.
Xylanses, microorganisms for its production, DNA molecules, proc of preparation and use thereof
L Patent: EP 0698667-A 2 28-FEB-1996;
SOLVAY (BE)
Other publication BE 1008751 960702
Other publication BE 809284 960105
Other publication FI 953578 960127
Other publication FI 953578 960127
Other publication AZ 2508695 960208.
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                                                                                 TATTTATGCGTCTATGGTTGGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGT
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                                121 AACAATGTTAACAACATGTTATTCGTAAAGGTAAAAATTCAATGAAACACAAAC
                                                                  TATTTATGCGTCTATGGTTGGACTGTTGACCCTCTTGTCGAATATTATATGTCGACAGT
                                                                                                                                                                                                TGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGGACCATCACTGTTGATGGAGGA
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    663
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Sequence 2 from Patent EP0698667.
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1 (bases 1 to 663)

S De, B.E., Lahaye, A., Ledoux, P. and Detroz, R.

Xylanase, microorganisms for its production, DNA molecules, process of preparation and use thereof

AL Patent: EP 069867-A 1 28-FEB-1996;

SOLVAY (BE)

Other publication BE 100875 960702

Other publication DR 9503454 960305

Other publication CR 2154628 960127

Other publication CR 2154628 960127

Other publication AU 2508695 960208.
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TTCCAGCCAAACGGTAATGCGTATTTATGCGTCTATGGTTGGACTGTTGACCCTCTTGTT 357
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                                GAATATTATATGCGACAGTTGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGG
                                                                                                                  418 ACCATCACTGTTGATGGAGGAACATATGATATCTATGAAACTCTTAGGAGTCAATCAGCCC
                                                                                                                                                                                  478 TCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGTGTCCGAAGATCGAAACGCACG
                                                                                                                                                                                                                                                     GTATATAGCAATAGCAATAAACGGAAACCCTCTCTCACAACTATAGTAATAAACGAG
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                                                           358 GAATATTATATTGTCGACAGTTGGGCGACTGCGTCCACCAGGAGCAACGCCTTAAGGGA
                                                                                               1100 TCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGTGTTCGAAGATCGAAACGCACG
                                                                                                                                                                                                                               AGTGGCACGATTTCTGTCAGCAACCACTTTAGAGCGTGGGGAAAACTTAGGGATGAATATG
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43.8%; Score 663; DB 6; Le
al Similarity 100.0%; Pred. No. 9.1e-124;
663; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                            1340 AGCATAACTTTGGATAAAAACAATTA 1365
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Sequence 1 from Patent BP0698667
A48222
A48222.1 GI:2302069
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De Buyl, E., Lahaye, A., Ledoux, P. and Detroz, R. Xylanase, microorganisms producing it, DNA molecules, preparing this xylanase and uses of the latter Patent: US 6346407-A 1 12-FEB-2002; Location/Qualifiers
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Xylanolytic enzyme; Bacillus agaradherens NCIMB 40482; breakdown; agricultural waste; alcohol fuel; enzymatic treatment; animal feed; release; free pentose sugar; dissolving pulp; cellulose; bio-bleaching; wood pulp; lignocellulostic material; animal feed additive; ss.
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                     used in treatment
                                                                                        A DNA sequence (AAT16102) coding for a xylanase precursor (AAR92054) wa isolated from a gene library of Bacillus sp. 72014 (LMG P-14798). The gene may be incorporated into a vector and expressed in transformed hosts, pref. Bacillus licheniformis or Bacillus pumilus, for prodn. of thermostable mature xylanase (AAR92053). The enzyme is useful in the paper pulp, animal feed and baking industries. (Updated on 16-OCT-2003 standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                        ATAGGAACTTTCCCATTTGCAAGACGATAAAAATCTTTTCCCCTATTTTATCTTATCG
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                   Bacillus derived xylanase active over wide pH ra of paper pulp, animal feeds and in bakery goods
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100.0%; Score 1513;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1513; Conservative 0; Mismatches
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                                                                                                                                                                                                                                       GTATATAGCAATACACTAAGAATTAACGGTAACCCTCTCTCAACTATTAGTAATGACGAG
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                                                                                                                                       601 GGGAAAATGTATGAAGTCGCGCTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAAT
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TCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGTGTTCGAAGATCGAAACGCACG
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95BE-00000448
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15-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a xylanolytic enzyme of Bacillus agaradherens NCIMB 40482. Xylanolytic enzymes are used for enzymatic breakdown of agricultural wastes for production of alcohol fuels, enzymatic treatment of animal feeds to release free pentose sugars, manufacturing of dissolving pulps yielding cellulose and bio-bleaching of wood pulp. They are also used for treatment of lignocellulostic material e.g. paper and pulp, or as an animal feed additive. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct PI field.)
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                                                                                                                                                                                                                                                                                                                      DNA construct encoding Bacillus agaradherens xylanolytic enzyme - and vectors and Bacillus cells containing these, useful for recombinant production of the enzyme for use in agricultural waste breakdown and lignocellulostic material treatment.
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                                                                                                                                                                                                                                 Olsen AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 840.6; DB 2;
Pred. No. 2.9e-188;
0; Mismatches 19;
                                                                                                                                                                                                                                 Schuelein M,
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Col 11-14; 10pp; English
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, Dambmann C;
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94US-00343600.
95US-00470398.
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milarity 97.8%;
Conservative 0
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P-PSDB; AAW60562.
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Best Local Similarity
Matches 852; Conserv
                                                                                                                                                                                                                                                Jorgensen PL,
                                                                                                              16-AUG-1996;
                                                                                                                                            02-JUL-1993;
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06-JUN-1995;
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                                                          A DNA sequence (AAT16102) coding for a xylanase precursor (AAR92054) was isolated from a gene library of Bacillus sp. 720/1 (LMG P-14798). The sequence (AAT16103) for the complete gene including 5' and 3' untranslated sequences was also obtd. The gene may be incorporated into a vector and expressed from either its own promoter or from the Bacillus pumilus PRL B12 promoter (see AAQ73996), and used for prodn. of recombinant thermostable xylanase in transformed hosts, pref. Bacillus licheniformis or B. pumilus The enzyme is useful in the paper-pulp, animal feed and baking industries. (Updated on 16-OCT-2003 to standardise
                                                                                                                                                                                                                                                                                                                                        619
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                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                       Score 744; DB 2; Le
Pred. No. 1.7e-165;
                                                                                                                                                                                                                                                                                                       0;
paper pulp, animal feeds and in bakery goods.
                                                                                                                                                                                                                                                                       Query Match 49.2%; Score 744; DB Best Local Similarity 100.0%; Pred. No. 1.7 Matches 744; Conservative 0; Mismatches
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                              Claim 9; Page 54-55; 94pp; English
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The present sequence encodes a polypeptide with xylanase activity used in an example of the present invention. The present invention describes a novel method for providing a novel DNA sequence encoding a polypeptide from a microorganism with an activity of interest. The method comprises:

(i) PCR amplification of the DNA with PCR primers with homology to (a) known gene(s) encoding a polypeptide with an activity of interest; (ii) linking the obtained PCR product of a 5' structural gene sequence and a 3' structural gene sequence, (iii) expressing the resulting hybrid DNA sequence; (iv) screening for hybrid DNA sequences encoding a polypeptide with the activity of interest or a related activity; and (v) isolating the hybrid DNA sequence identified in step (iv). This method provides for having to cultivate and isolate the microorganism without
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolating novel DNA sequences from microorganisms - without the need for culturing the microorganism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGC
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                                                                                                                                                                 Glycosyl hydrolase family 11 xylanase DNA derived from Bacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "glycosyl hydrolase family 11 xylanase"
                                                                                                                                                                                                                     Bacillus sp; xylanase; glycosyl hydrolase family 11; isolation; microorganism; identification; ss.
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Pred. No. 2.5e-158;
0; Mismatches 19;
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                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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AAV13067 standard;
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-PSDB; AAR76551
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                                                                                                                                                                                                                                GGGAAAATGTATGAAGTCGCGCTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAAT
                                                                                                                                                                                                                                                                     thermostable alkaline endo-1,4-beta-D-xylanase gene; cloning;
polymerase chain reaction; Escherichia coli; EC-3.2.1.8; paper; pulp;
bleaching; de.
          TCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGTGTTCGAAGATCGAAACGCACG
                                    | TTCAATGAAACACAAACAACCAACAAGTTGGTAACATGTCCATAAACTACGGAGCCAAC
                                                                        TTCCAACCAAATGGTAATGTTTTATGCGTCTATGGTTGGACTGTTGACCTTTGTC
                                                                                                                     GAATATTATATTGTCGATAGTTGGGGCAACTGGCGTCCACCAGGGGCAACGCCTAAGGA
                                                                                                                                                         ACCATCACTGTTGATGGAGGAACATATGATCTATGAAACTCTTAGAGTCAATCAGCCC
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Quax WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Van Solingen P, Williams DP, Iverson S, Farrell RL, Van Der Kleij WA, Herweijer MA, Van Beckhoven RFWC, Goedegebuur F, Jones BE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermostable alkaline endo-1,4-beta-D-xylanase gene
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                                                                                                                                                                                                                                                                                                                                                    744
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                  AAQ92878 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-DEC-1994;
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12-FEB-1996
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                                                                                                             The sequence encodes an alkaline endo-1,4-beta-D-xylanase (G-type) from Bacillus sp. 1-43-3. Fragments of the sequence (e.g. the internal fragments given in AAQ92877) may be amplified by polymerase chain reaction, e.g. using piners with sequences AAQ92865, AAQ92867, AAQ92868 and AAQ92869. The DNA may be cloned in Escherichia coli using a plasmid vector for recombinant xylanase production. The xylanase may be used in the paper and pulp industries, where it produces an increase its obtains so is seftwood pulp of at least 1.0 over non-enzymatically treated pulp in an ECF pulp bleaching process, at pH 9.0 and 65 deg C. The enzyme may be used in production of paper, board and fluff pulp, and has low cellulase activity. The increased brightness produced using the xylanase allows reduction in the amount of bleaching chemicals used.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57
ph - useful in paper and pulp prodn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTACGTTCAGTGCCCAATGGAACAATGTTAACAACATATTATTCCGTAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 744 BP; 248 A; 145 C; 159 G; 192 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 44.5%; Score 673.6; DB 2; Il Similarity 95.7%; Pred. No. 6.8e-149; 714; Conservative 0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                               (Updated on 16-OCT-2003 to standardise OS field)
  xylanase enzyme active at high
                                                                           Claim 4; Page 42-43; 54pp; English
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CTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAATGTATATAGCAATACACTAAGA 1300
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 GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGCCGGTACGTTCAGTGCCCAATGG 120
                                                           ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACA
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                                     TTTAAACAATATTGGAGTGTTCGAAGATCGAAACGCACGAGGGCACGATTTCTGTCAGC
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                                                                                                                                                                                                                                              TGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGA
                                                                                                                                                                                                                                                                             301 TGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGA
                                                                                                                                                                                                                                                                                                                 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGGATTGCCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "positive clone for xylanase activity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus sp; xylanase; glycosyl hydrolase family 11; isolation; microorganism; identification; hybrid DNA; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xylanase activity positive clone DNA SEQ ID NO:11
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1. .747
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/product=
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Bacillus sp.
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658 GTATATAGGAATACACTAAGAATTAACGGAAACCCTCTCTCAACTATTAGTAATAACGAG 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to standardise
                                                                                                                                                                                                                                                                                                             Xylanase; thermostable enzyme; paper; pulp; bleaching; feedstuff; baking;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus derived xylanase active over wide pH range - used in treatment of paper pulp, animal feeds and in bakery goods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (I_MG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A DNA sequence (AAT16101) coding for a thermostable mature xylanase (AAR92053) was isolated from a gene library of Bacillus sp. 720/1 (LMG 14798). Sequences were also obtd. (see AAT16102 and AAT16103) for the xylanase precursor and for the complete gene including 5' and 3' untranalated sequences. DNA coding for the mature enzyme may be incorporated into a vector and expressed from either its own promoter from the Bacillus pumilus PRL B12 promoter (AAQ73996), and used for prodn. of recombinant xylanase in transformed hosts, pref. Bacillus licheniformis or B. pumilus. The enzyme is useful in the paper-pulp, animal feed and baking industries. (Updated on 16-OCT-2003 to standard)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CAAATGGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGG
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2.1e-146;
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                                1340 AGCATAACTTTGGATAAAACAATTA 1365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.8%; Score 663; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                Bacillus sp; strain 710/1 (LMG P-14798)
                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/EC_number= "3.2.1.8"
                                                                  AGCATAACTCTAGATAAAAACAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 30; Page 50-51; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .663
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Conservative 0;
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95BE-00000448
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P-PSDB; AAR92053.
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663; Conserv
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                                                                                                                                                                                                                                                                             Xylanase gene
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17-MAY-1995;
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15-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                540
                                                                                                                      The present sequence represents a positive clone for xylanase activity from an example of the present invention. The present invention describes a novel method for providing a novel DNA sequence encoding a polypeptide from a microorganism with an activity of interest. The method comprises: (i) PCR amplification of the DNA with PCR primers with homology to (a) known gene(s) encoding a polypeptide with an activity of interest; (ii) linking the obtained PCR product of a 5' structural gene sequence and a 3' structural gene sequence (iii) expressing the resulting hybrid DNA sequence; (iv) screening for hybrid DNA sequences encoding a polypeptide with the activity of interest or a related activity; and (v) isolating the hybrid DNA sequence identified in step (iv). This method provides for identification and isolation of sequences from microorganisms without having to cultivate and isolate the microorganism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 GAATATTATATTCTCGATAGTTGGGGCAACTGGCGTCCACCAGGGGAACGCCTAAGGGA 420
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                                                           novel DNA sequences from microorganisms the microorganism.
                                                                                                                                                                                                                                                                                                                                  Score 590.2; DB 2;
Pred. No. 3.2e-129;
                                                                                                                                                                                                                                                                                                                                                             98;
          Kauppinen
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          Sandal T,
                                                                                                Example 1; Page 35; 72pp; English.
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            Diderichsen B,
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Best Local Similarity 86.9
Matches 649; Conservative
                                  WPI; 1998-008878/01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   620 AIGAGACAAAAGAAATIGACGITGAITITTAGCCITITITAGITITGCACIAACCITA 679
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1280 GTATATAGCAATACACTAAGAATTAACGGTAACCCTCTCTCAACTATTAGTAATGACGAG
                                      Novel xylanase recombinant polypeptide useful for improving textile texture, treating paper, eliminating microorganisms.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding xylanase from an environmental sample seq id 163.
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Esteghlalian A;
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                                                                                                                                                               Claim 1; SEQ ID NO 163; 570pp; English.
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ACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGT 1138
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EC_number= "3.2.1.8"
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                             /note= "claim 10"
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Best Local Similarity 62.1
Matches 481, Conservative
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Bacillus licheniformis; ss.
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/note= "claim 12"
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186. :869
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bleaching;
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                                                                                                                                                                                                        Purified xylanase from Bacillus pumilus PRL B12 - esp. produced in transformed Bacillus licheniformis, and related DNA, vectors, etc., used for pre-treatment of wood pulp to reduce chlorine or ozone consumption in subsequent bleaching.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               779 ACAATGATTCTCAATCATGGGGGTACGTTCAGTGCCCAATGGAACAATGTTAACAACATA 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTATTCCGTAAAGGTAAAAATTCAATGAAACACAAAACACCAACAACAAGTTGGTAACATG 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   462 TCCATCAACTACAACGCAGCCTTTAACCCGGGCGGGAATTCCTATTTATGTGTCTATGGC 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Bacillus pumilus PTL B12 (ATCC 55443) gene library was screened for recombinant plasmids carrying the xylanase gene. A chromosomal fragment obtained from isolate BDRM was subcloned and expressed in Escherichia coli JM109. The sequence of the xylanase gene (as a 1022 bp Sau3AI fragment) carried by a selected transformant is given in AAQ80923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCGATGACACTCAATAACGGGGGGCATTTAGTGCAAGCTGGAACAATATTGGAAATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         719 TCCATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225 ATTGGATTTGTGCTGACACTGACGGCTGTGCCGGCTCATGCGGAAACGATTTATGATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATTAAAAGGAGGAATGCCTAATGAGACAAAGAAATTGACGTTGATTTTAGCCTTTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    659 GTTTGTTTTGCACTAACCTTACCTGCAGAAATAATTCAGGCACAAATCGTCACCGACAAT
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    Ledoux
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1022 BP; 329 A; 197 C; 229 G; 266 T; 0 U; 1 Other;
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    Lahaye
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Detroz
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284 778 958

461

401

Length 1956;

DB 12;

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The invention describes an isolated or recombinant polypeptide (I), having 50% or more identity to 190 300-1200 residue amino acid sequences (SI), given in the specification, over a region of 100 or more residues and the polypeptide as thermostable xylanase activity. (I) is useful for: dough conditioning; beverage production; as a nutritional supplement in animal feed; reducing lignin in a wood or a wood product; and for eliminating and protecting animals from a microorganism comprising xylan. The polynucleotide (II) encoding (I) is useful for amplifying nucleic acid encoding a polypeptide having a xylanase activity which involves amplifying (II) or its subsequence. (I) is useful for treating and preventing bacterial infection and fungal infection e.g. coccidiosis. This sequence encodes xylanase protein isolated from an environmental
                                                                                                                                                                    CAAAGTAGCGGAAGTGCTAATGTATATAGCAATACACTAAGAATTAACGGTAACCCTCTC 1318
                                                                                                   GAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCGCTTACTGTAGAAGGCTAT 1258
                                                                                                                                                                                                      878
                                                                   758
                                                                                                                                    818
ACGCTCCGTGTCAATCAGCCTTCTATCGAGACGCTACCTTCAAACAATATTGGAGT 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibacterial; fungicide; thermostable xylanase activity; dough conditioning; beverage production; nutritional supplement; animal feed; lignin reduction; wood product; xylan; bacterial infection; fungal infection; coccidiosis; gene; ds.
                                                                                                                            819 cgaaccaaccaacreccaarcrearcaccaarcaccrearcarrarrearra
                                 GTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGCAACCACTTTAGAGCGTGG
                                                                 GTACGTCAAACAAACGCACAAGCGGAACGGTCTCCGTCAGTGAGCATTTTAAAAAATGG
                                                                                                                                                                                                                                      1319 TCAACTATTAGTAATGACGAGGCATAACTTTGGATAAAAACAATTAAAAATCC 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel xylanase recombinant polypeptide useful for improving textile texture, treating paper, eliminating microorganisms.
                                                                                                                                                                                                                                                                      DNA encoding xylanase from an environmental sample seq id 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 267; 570pp; English
                                                                                                                                                                                                                                                                                                                                                             ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Callen W, Healey S,
                                                                                                                                                                                                                                                                                                                                                               ADJ35051 standard; DNA; 1956
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Esteghlalian A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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Sequence 1956 BP; 614 A; 384 C; 423 G; 535 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                             AAATGGTAATGCGTATTTATGCGTCTATGGTTGGACTGTTGACCCTCTTGTCGAATATTA 987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibacterial; fungicide; thermostable xylanase activity;
dough conditioning; beverage production; nutritional supplement;
animal feed; lignin reduction; wood product; xylan; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTATGAAGTCGCGCTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAATGTATATAG
                                                                                                                                                                                          198 TAGTTGTCAATGGAGTAATACGGTAATGCACTATTTAGAAAAGGGAGAAAATTTAATTC
                                                                                                                                                                                                                                                                                                      318 AAACGGAAATTCCTATTTGTGTGTTTACGGTTGGACAAGAAATCCACTGGTTGAATATTA
                                                                                                                                                                                                                                                                                                                                      988 TATTGTCGACAGTTGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      558 AATATCTGTCACTGAACATTTTAAACAGTGGGAAAGAATGGGCATGCGAATGGGTAAGAT
                                                                                                                                       TGAGCTCTGGAAAGA----CTACGGAAATACGATTATGGAACTTAACGACGGTGGTACTTT
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                                                                                                                                                                                                                                                  ceacaaaaccrarcaacaarraaccacararacracracaararccaararacaarcc
                                                                                                                                                                                                                                                                                                                                                        438 AGIGGAIGGCGGIACTIAIGAAATATATGAAACTACCCGGGTAAATCAGCCTTCCATCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGTGCCCAATGGAACAATGTTAACAACATATTATTCCGTAAAAGGTAAAAATTCAATGA
                                                                                                           TGAATTTTGGAAAGATAGCGGTGGCTCTGGGACAATGATTCTCCAATCATGGCGGTACGTT
                                                   AATAATTCAGGCACAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTA
                          Gaps
                         3;
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                          Indels
Score 276.6; DB 12;
Pred. No. 3.8e-55;
0; Mismatches 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1314
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 18.3%;
66.2%;
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  Query Match 18.3
Best Local Similarity 66.2
Matches 415; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADJ34969 standard;
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Xylanase A; XynA; cellulosome; feruloyl esterase; phenolic acid esterase;
thermostable; ferulic acid; wheat bran; agricultural byproduct; treat;
grass; paper and pulp industry; feed processing; food additive;
plant cell wall material; degradation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant DNA molecule comprising a sequence encoding feruloyl esterase protein, useful for treating grasses and other plant materials used in pulp and paper industries, feed processing and food additives.
                                                          Li X, Ljungdahl LG;
                                                                                                                                                                                                                                                                               Clostridium stercorarium xylanase A DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 97-99; 105pp; English.
                                                                                                   1280 GTATATAGCAATACACTAAGAATT 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Xylanase A"
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                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 440. .1978
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                                                                                                                           Grcargacgaarcagcrgargarr
                                                                                                                                                                                                BP.
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/product= '
                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-256991/22.
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                                                                                                                              655
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                                                                                                                                                                      RESULT 12
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                                                                                                                                                                                    AAZ51821
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                                                                                                                                                                                                       The invention describes an isolated or recombinant polypeptide (I), having 50% or more identity to 190 300-1200 residue amino acid sequences (S1), given in the specification, over a region of 100 or more residues and the polypeptide as thermostable xylanase activity. (I) is useful for: dough conditioning, beverage production, as a nutritional supplement in animal feed; reducing lignin in a wood or a wood product; and for eliminating and protecting animals from a microorganism comprising xylan. The polynucleotide (II) encoding (I) is useful for amplifying nucleic acid encoding a polypeptide having a xylanase activity which involves amplifying (II) or its subsequence. (I) is useful for treating and preventing bacterial infection and fungal infection e.g. coccidiosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   620 ATGAGACAAAAGAAATTGACGTTGATTTTAGCCTTTTTAGTTTTGCTTTAGCTTAACCTTA
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                                                                                                                                         it polypeptide useful for improving textile eliminating microorganisms.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 684 BP; 221 A; 129 C; 158 G; 176 T; 0 U; 0 Other;
                                                         Blum
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Pred. No. 9.5e-55;
                                                         Hazlewood G,
                                                                                                                                                                                 Claim 1; SEQ ID NO 185; 570pp; English
                                                         ς,
  14-JUN-2002; 2002US-0389299P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                18.1%;
64.6%;
                                                          Healey
                                                                                                                                           recombinant
                                                                                                                                                         texture, treating paper,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 442; Conservative
                              (DIVE-) DIVERSA CORP
                                                                                                WPI; 2004-099016/10.
P-PSDB; ADJ34970.
                                                         Callen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                      Esteghlalian A;
                                                                                                                                            xylanase
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The present sequence is a DNA encoding xylanase A (XynA) from Clostridium stercorarium. XynA contains family VI cellulose binding domain (CBD) which is homologous to the CBD of xylanase Z (XynZ) of Clostridium thermocellum. XynZ is an enzymatic component of C. thermocellum cellulosome and has a multi-domain structure which includes a dockerin domain, a catalyvic xylanase domain, a family VI cellulose binding domain and a domain of unknown function. The unknown domain in the N-terminal region of XynZ has been found to contain feruloy! (phenolic acid) esterase which is involved in the degradation of plant cell wall material. The novel feruloyl esterase is thermostable, easy to purify, has high temperature optima and stable over a wide pH range. The enzyme is used for producing ferulic acid from wheat bran or agricultural byproducts, treating grasses or other plant materials used in the pulp and paper industries, in feed processing and as a food additive DB 3; Length 2364; Sequence 2364 BP; 791 A; 428 C; 458 G; 687 T; 0 U; 0 Other; Score 255.6; 16.9%; Query Match

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WO9736995-A2
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G-Xylanase; beta -1,4-xylanase activity; activity; thermal stability;
biological bleaching; cellulose product; paper pulp; ss.
                                                                                                                                                                                                               757 AAAceeAAArrccrArrrerererrrAceerreeAcaAGAAArccaCreereAArerrA
                                                                                                                                                                                                                                                         817 CATTGTAGAAAGCTGGGGCAGCTGGGCGTCCACCTGGAGCAACACCCAAAGGAACCATCAC
                                                                                                                                                                       cgacaaaaccrarcaagaarraagagacaragargargararargarargarragarracaarcc
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                                                 520 AGTACTCGCCGGCGAATAATTTACGACAATGAGACAGGCACACATGGAGGCTACGACTA
                                                                      748 TGAATTTTGGAAAGATAGCGGTGGCTCTGGGACAATGATTCTCAAATCATGGCGGTACGTT
                                                                                        580 igagcicrogaaaga---cracogaaajacoarrarogaaciraacoacoorograciri
                                                                                                              808 CAGIGCCCAAIGGAACAAIGIIAACAACAIAIIAIICCGIAAAAGGIAAAAAIICAAIGA
                                                                                                                                                     868 AACACAAACACACCAACAAGTTGGTAACATGTCCATAAACTACGGAGCCAACTTCCAACC
                                                                                                                                                                                              AAATGGTAATGCGTATTATGCGTCTATGGTTGGACTGTTGACCCTTGTTGAATATTA
           Gaps
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          Indels
 Pred. No. 3.6e-50;
0; Mismatches 214;
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           410, Conservative
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 Best Local Similarity
Matches 410; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a RT46B.1 xynB gene and encodes a xylanse enzyme. The present sequence is derived from a gene contained within Dictyoglomus thermophilum strain Rt46B.1. The xylanase is contained within the family of enzymes known as G-xylanases, and has beta -1,4-xylanase activity. The enzyme has high activity and high thermal stability with optimum activity at 85 degrees Celcius and pH 6.5. The xylanase enzyme is used for the biological bleaching of cellulose products, especially paper pulp. Use of the enzyme ensures that waste streams from the biological bleaching will include less toxic material
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Pred. No. 3.4e-41;
0; Mismatches 278; Indels 9;
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59.0%;
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27-MAR-1997;
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GGAGTGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGCAACCACTTTAGAG 1193
                                                                   691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A full-length xynD gene (AAT08142) codes for a thermostable G-type xylanase (AAR87012) useful in the pulp and paper industries. The gene was obtd. by genomic walking PCR of DNA from an extremely thermophilic bacterium, strain TG456 (CBS 213:94), isolated from a New Zealand hot spring. The gene can be inserted into a vector and used for the prodn. of recombinant xylanase D in microbial host cells, esp. Escherichia coli. (Updated on 25-MAR-2003 to correct OS field.)
                      631
                     572 GGAGTGTAAGGACATCTAAGAGAACAAGTGGAACAGTCACTGTAACAGATCACTTTAGGG
                                             CGTGGGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCGCTTACTGTAGAAG
                                                                 632 Cariciccaaaragagirriaaacciriceracratricaarcaariracriricicirigaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel xylanase(s) having activity at 80 deg.C. or higher - obtained franaerobic thermophilic bacteria and used in paper and pulp production processes.
                                                                                                                                                                                                                                                                                  Xylanase D; xynD gene; thermostable enzyme; paper; pulp; lignin;
delignification; xylan; bleaching; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 1244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1244 BP; 380 A; 215 C; 279 G; 360 T; 0 U; 10 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moody D;
Quax WJ;
                                                                                        GCTATCAAAGTAGCGGAAGTGCTAATGTATATAGCAATAC 1293
                                                                                                             GATATCAAAGCAGTGGTTCGGCTAATATAACACAAAATAC 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Forster S,
Morgan HW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 204.8; DB 2;
Pred. No. 2.9e-38;
2; Mismatches 224;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Iverson S,
Daniel RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 9; Page 56-58; 77pp; English.
                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1..1107
/*tag= a
                                                                                                                                                                     BP
                                                                                                                                                                    AAT08142 standard; DNA; 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                   95WO-EP002299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        94EP-00201699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 13.5%;
Best Local Similarity 61.0%;
Matches 367; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Groenberg V, Williams DP,
Farrel RL, Bergquist PL,
Herweijer MA, Jones BE;
                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KONN ) GIST-BROCADES BV.
                                                                                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-049690/05.
P-PSDB; AAR87012.
                                                                                                                                                                                                                                                            Xylanase xynD gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JUN-1994;
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12-MAY-1996
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TTACCTCTAATGCAACTGGGACATACGATGGTTACTACGAGTTGTGGGAAGACACAG 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibacterial; fungicide; thermostable xylanase activity; dough conditioning; beverage production; nutritional supplement; animal feed; lignin reduction; wood product; xylan; bacterial infection; fungal infection; coccidiosis; gene; ds.
                                                        GTGGCTCTGGGACAATGATTCTCAATTCATGGCGGTACGTTCAGTGCCCAATGGAACAATG
                                                                                    1128 AATATTGGAGTGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGCAACCACT
                                                                                                                                 TTAACAACATATTATTCCGTAAAGGTAAAAATTCAATGAAACACAAAAACACACAACAAG
                                                                                                                                                                    188 TTAACAATGCACTCTTCAGAACAGGTAAAAAGTTTAGCACTGCATGGAATCAGC-----
                                                                                                                                                                                                        948 GCGTCTATGGTTGGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGTTGGGGCA
                                                                                                                                                                                                                                                                                                                   302 dcarrranddardcrcaagaaarccacrrgraaarrrranarcgrgaaagcregggcr
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                                                                                                                                                                                                                                             242 TTGGGACTGTAAAGATTACCTACTTGCTACCTACAATCCAAATGGCAATTCCTATCTCT
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Esteghlalian A;

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Indels

TCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAAGATAGCG 767

708

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having 50% or more identity to 190 300-1200 residue amino acid sequences (S1), given in the specification, over a region of 100 or more residues and the polypepitde as thermostable xylamase activity. (I) is useful for dough conditioning, beverage production, as a nutritional supplement in animal feed; reducing lignin in a wood or a wood product; and for eliminating and protecting animals from a microorganism comprising xylan. The polynucleotide (II) encoding (I) is useful for amplifying nucleic acid encoding a polypeptide having a xylamase activity which involves amplification of a template nucleic acid with a primer pair capable of amplifying (II) or its subsequence. (I) is useful for treating and preventing bacterial infection and fungal infection e.g. coccidiosis. This sequence encodes xylamase protein isolated from an environmental
                                                                                     Novel xylanase recombinant polypeptide useful for improving textile texture, treating paper, eliminating microorganisms.
                                                                                                                                                                                                                   an isolated or recombinant polypeptide (I)
                                                                                                                                                               Claim 1; SEQ ID NO 227; 570pp; English
                                                                                                                                                                                                                      The invention describes
                  WPI; 2004-099016/10.
P-PSDB; ADJ35012.
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Sequence 747 BP; 174 A; 222 C; 244 G; 107 T; 0 U; 0 Other;

1193 GCGTGGGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCGCTTACTGTAGAA 1252 1013 CGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGAACATATGATATC 1072 1073 TACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATTTAAACAATAT 1132 1133 TGGAGTGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGCAACCACTTTAGA 1192 519 893 AACATGTCCATAAACTACGGAGCCAACTTCCAACCAAATGGTAATGCGTATTTATGCGTC 952 340 AATCAGACGTGACCTACCAGGCAAACTACCAGCCGAACGGCAATTCATACCTGTGCGTA 399 459 TACCGCACCCAGCGCGTCAACCAGCCTTCCAACGAGCCACCAAGACCTTCTATCAATAC 579 580 regadeciricecacreagaageceaceaegegegaaceareaegreegerreececreacreere 639 640 GCCTGGGCGACGAAGGGGATGAACATGGGGAGTCTGTACGAGGTGTCGATGACGTCGAG 699 460 ceccecesesesaacercaresecacercaresecaceseseseseseseseses Gaps ô Score 177.8; DB 12; Length 747; Pred. No. 5.9e-32; 0; Mismatches 132; Indels 0; GCCTATCAAAGTAGCGGAAGTGCTAATGT 1281 11.8%; 66.1%; Query Match 11.8 Best Local Similarity 66.1 Matches 257; Conservative 520 1253 g g 셤 ò 요 ઠે g ઠે ઠે 셤 ઠ ઠે

Search completed: November 10, 2004, 17:09:33 Job time: 962.753 secs

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Sequence 1,
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Sequence 32,
Sequence 30,
Sequence 32,
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Sequence 3
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                          GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-470-953A-5

US-08-189-060B-1

US-08-10-126-18

US-08-470-953A-12

US-08-470-953A-12

US-08-470-953A-12

US-08-470-953A-12

US-08-275-526C-1

US-08-275-526C-1

US-09-076-677-1

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US-09-076-677-1

US-09-073-055-1

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Maximum Match 100%
Listing first 45 summaries
                                                                                                                    nucleic search, using sw model
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28 255 16.9 600 4 US-09-076-677-26 Sequence 26, Appl 29 255 16.9 600 4 US-09-076-677-34 Sequence 34, Appl 30 255 16.9 600 4 US-09-076-677-34 Sequence 34, Appl 31 255 16.9 600 4 US-09-073-055-26 Sequence 26, Appl 32 204.8 13.5 1244 3 US-08-591-685-12 Sequence 12, Appl 34 154.4 10.2 164 3 US-08-501-126-15 Sequence 12, Appl 35 150 9.9 150 3 US-08-501-126-15 Sequence 13, Appl 36 132.4 8.8 294 3 US-08-501-126-16 Sequence 13, Appl 37 132.4 8.8 294 3 US-08-470-9334-1 Sequence 14, Appl 39 119.4 7.9 1375 3 US-08-590-563-1 Sequence 1, Appl 39 119.4 7.9 1375 4 US-09-235-031-1 Sequence 1, Appl 24 119.4 7.9 1375 4 US-09-235-031-1 Sequence 1, Appl 24 119.4 7.9 1375 4 US-09-235-031-1 Sequence 1, Appl 39 119.4 7.9 1375 4 US-09-235-031-1 Sequence 1, Appl 41 119.4 7.9 1375 4 US-09-235-031-1 Sequence 1, Appl 41 119.4 7.8 573 1 US-08-90-912-18 Sequence 1, Appl 41 118.4 7.8 573 1 US-08-709-912-18 Sequence 18, Appl 44 118.4 7.8 1207 1 US-08-70-912-18 Sequence 2, Appl 45 117.8 7.9 1207 1 US-08-57-964-2
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ALIGNMENTS

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RESULT 1

RESULT 1

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RESULT 1

RESULT 1

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RESULT 1

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RESULT 1

RESULT 1

RESULT 2

REPLICANT: EXIC DE BUYL

APPLICANT: RENE BLANZE

APPLICANT: RENE DETROX

TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase

TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase

TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase

TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase

TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase

TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase

TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase

COUNTY: Washington X molecule and the compatible

STATE: 20006

COUNTY: Washington X SE., N.W., Suite 200

STATE: 20006

COUNTY: U.S.A.

TITLE OF STATES PREMEDIA PORN

MEDIUM TYPE: Flopy disk

COMPUTER: INPERIOR COMPATION:

MEDIUM TYPE: Flopy disk

COUNTY: GOOD NATE: DOSS/MS-DOS

SOFTWARE PAREIT Release #1.0, Version #1.25

COUNTY: APPLICATION DATE:

RELIGIORATION NATE:

ATRONARY/AGENT INFORMATION:

RESISTATION NUMBER: A111-40

TILLECOMMUNICATION NUMBER: 4111-40

TILLECOMMUNICATION INFORMATION:

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RESULT 2
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Squence 11, Application US/08470953A
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Squence 11, Application US/08470953A
Squence 11, Application US/08470953A
SAPLICANT: BANDRE LAHAYE
APPLICANT: RENE DETROZ
TITLE OF INVENTION: Xylanase, microorganisms produced it,
TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase;
TITLE OF INVENTION: and uses thereof
TITLE OF INVENTION: and uses thereof
UNUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE
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                                                                                                                                                                                                  1261 AAGTAGCGGAAGTGCTAATGTATATAGCAATACACTAAGAATTAACGGTAACCCTCTCTC
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                                                   TCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGTGT
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MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: Ploppy disk
COMPUTER: Plan PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,953A
FILING DATE: 6-OCTOBER-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136

, REFERENCE/DOCKET NUMBER: 4121-40
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COUNTRY: U.S.A.
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                                                                    AAATTGAATTGTGTATATCTAATGATAACGACAAATCGTCACTGTTTTTAAACTAATCTC
                                                                                   AAACCAATACTTCTTTATTTAACGCTAACCACTTGCAATCTTATCACAAGAACATTCTTT
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Query Match 100.0%; Score 1513; Best Local Similarity 100.0%; Pred. No. 0; Matches 1513; Conservative 0; Mismatches
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TCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGTGT
                                         CATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGGAC
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Patent No. 5770424

GENERAL INFORMATION:

APPLICANT: Outtrup, Helle
APPLICANT: Dambmann, Claus
APPLICANT: Olsen, Arne Agerlin
APPLICANT: Sch lein, Martin
APPLICANT: Sch lein, Martin
APPLICANT: Sch lein, Per Lina
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                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1513; Conservative 0; Mismatches
      TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1513 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                          MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Bacillus
                                                                                                                                                                                                                                                    LOCATION: 701..1363
FEATURE:
NAME/KEY: 8ig_peptide
LOCATION: 620..700
                                                                                                                                                                                                                                        mat_peptide
701..1363
                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 620..1363
FEATURE:
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                                                                                                                                                                                                                                        NAME/KEY:
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Patent No. 6346407
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ANDREE LAHAYE
APPLICANT: RIENE DEDOUX
APPLICANT: RENE DETROZ
TITLE OF INVENTION: Xylanase, microorganisms produced it,
TITLE OF INVENTION: And uses thereof
TITLE OF INVENTION: and uses thereof
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE

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                                                                      GAATATTATATTGTCGACAGTTGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGG 1039
                                                                                                                                                         1100 TCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGTGTTCGAAGGATCGAAACGCACG 1159
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  TTCCAGCCAAACGGAAATGCGTATTTATGCGTCTATGGTTGGACTGTTGACCTCTTGTC 360
                                                                                                                                                                                  421 ACCATCACTGTTGATGGAGGAACATATGATGATGTATGAAACTCTTAGAGTCAATCAGCCC
                                                                                                                                                                                                                                                                      661 GTATATAGCAATACACTAAGAATTAACGGTAACCCTCTCTCAACTATTAGTAATGACAAG
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COUNTRY: U.S.A.

COUNTRY: U.S.A.

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/470,953A

FILING DATE: 6-OCTOBER-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING BATE:

ATTORNEY/AGENT INFORMATION:
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; Sequence 4, Application US/08470953A
; Patent No. 6346407
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                                          No. 57704240 No. 5770424disk of No. 5770424th America, Inc
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                                                                                                                                                                                                                                               DB 1;
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Pred. No. 5.8e-216;
0; Mismatches 19;
                                 STATES No. 57704240 No. 5770424disk of STREET: 405 Lexington Avenue, Suite 6400 CITY: New York STATE: New York STATE: New York COUNTRY: U.S.A. ZIP: 10174-6401 COMPUTER FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Bacillus agaradherens
STRAIN: NCIMB 40482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 55.6%;
Best Local Similarity 97.8%;
Matches 852; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 871 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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APPLICANT: ANDREE LAHAYE
APPLICANT: ANDREE LAHAYE
APPLICANT: BERT DE BUYL
APPLICANT: PIERRE LEDOUX
APPLICANT: PIERRE LEDOUX
TITLE OF INVENTION: Xylanase, microorganisms produced it,
TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase
TITLE OF INVENTION: and uses thereof
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CCTGCAGADATADATTCAGGCACAAATCGTCACCGACAATTCCATTGGCAACCACGATGGC 120
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: EN PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,953A
FILING DATE: G-OCTOBER-1995
CLASSIFICATION NUMBER:
APPLICATION NUMBER:
PILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 49.2%; Score 744; DB 3; Lv Best Local Similarity 100.0%; Pred. No. 4.6e-190; Matches 744; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                             E: WILLIAN BRINKS HOFER GILSON & LIONE 2000 K St., N.W., Suite 200
                                                           US-08-470-953A-5; Sequence 5, Application US/08470953A; Patent No. 6346407; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 4121
TELECOMMUNICATION INFORMATION:
TELEPRONE: 202-429-6625
TELERX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Ee
REGISTRATION NUMBER: 37,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 744 base pairs
nucleic acid
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1..81
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82..744
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LOCATION:
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US-08-470-953A-5
                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                   Query Match 49.2%; Score 744; DB 3; Le Best Local Similarity 100.0%; Pred. No. 4.6e-190; Matches 744; Conservative 0; Mismatches 0;
NAME: Wilhlem F. Gactaux, ---
REGISTRATION NUMBER: 37,136
REPERRICE/CONCET UNMBER: 4121-40
TELECOMMUNICATION INPORMATION:
TELEPHONE: 202-429-0625
TELEFAX: 6202 293-1850
TELEFAX: 650 383-5605
INPORMATION FOR SEQ ID NO: 5EQUENCE CHARACTERISTICS: LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1340 AGCATAACTTTGGATAAAACAAT 1363
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MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Bacillus
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); Mismatches 19;
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97.48;
                Conservative
 Best Local Similarity
                725;
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                                                                                         181 GGTACGTTCAGTGCCCAATGGAACAATGTTAACAACATATTATTCCGTAAAAGGTAAAAAA
                                                                                                                                                       481 TCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGTGTTCGAAGATCGAAACGCACG
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Patent No. 6270968

GENERAL INFORMATION:

APPLICANT: Dalboge, Henrik

APPLICANT: Sandal, Thomas

APPLICANT: Barge, Diderichsen

ITILE OF INVENTION: Method Of Providing No. 6270968el DNA Sequences

FILE REFERENCE: 4772.204-08

CURRENT APPLICATION NUMBER: US/09/189,060B

CURRENT APPLICATION NUMBER: US/09/189,060B

PRIOR FILING DATE: 1997-05-12

NUMBER OF SEQ ID NOS: 74

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 744
                                                                         800 GGTACGTTCAGTGCCCAATGGAACAATGTTAACAACATATTATTCCGTAAAGGTAAAAAA
                                                                                                                                     TTCAATGAAACACAACACACCAACAAGTTGGTAACATGTCCATAAACTACGGAGCCAAC
                                                                                                                                                                                                TTCCAACCAAATGGTAATGCGTATTAATGCGTCTATGGACTGGTTGACCCTCTTGTC
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NAME/KEY: CDS;
LOCATION: (1).
US-09-189-060B-1
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Williams, Diane P.

Iverson, Sara
Iverson, Sara
Farrell, Roberta L.
Harbes, Wilhelmina T.
Van Der Kleij, Wilhelmus A.
Herweijer, Margaretha A.
Van Beckhoven W.C., Rudolf F.
Ones, Wilhelmus J.
Jones, Wilhelmus J.
  APPLICANT: Van Solings
APPLICANT: Williams, I
APPLICANT: Farrell, R
APPLICANT: Herbes, Wil
APPLICANT: Wan Der Kie
APPLICANT: Wan Becklow
APPLICANT: Van Becklow
APPLICANT: Van Becklow
APPLICANT: Ouax, Wilhs
APPLICANT: Jones, Wilhs
APPLICANT: Jones, Wilhs
APPLICANT: Jones, Wilhs
APPLICANT: Jones, Wilhs
APPLICANT: Jones, Wilhs
APPLICANT: Jones, Wilhs
APPLICANT: Jones, Brief
TITLE OF INVENTION: Brief
MUMBER OF SEQUENCES: 2
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APPLICANT: ANDREE LAHAYE
APPLICANT: ERIC DE BUYL
APPLICANT: PIERRE LEDOUX
APPLICANT: PIERRE LEDOUX
TITLE OF INVENTION: Xylanase, microorganisms produced it,
TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase
TITLE OF INVENTION: and uses thereof
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE
                                                                                                                                                                                                                                                                                                             1280 GTATATAGCAATACACTAAGAATTAACGGTAACCCTCTCTCAACTATTAGTAATGACGAG 1339
                                                                                                                                                                                                                                 1220 GGGAAAATGTATGAAGTCGCGCTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAAT 1279
                                                                                                  538 AGTGGCACAATTTCTGTCAGCAACCACTTTAGAGCGTGGGAAAACTTAGGGATGAACATG 597
                                                                                                                                                                                                                                                         TCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGTGTTCGAAGATCGAAACGCACG
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418 ACCATCACTGTTGATGGAGGAACATATGATATCTATGAACTCTTAGAGTCAATCAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.

ZIP: 20006
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATENT PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,953A
FILING DATE: 6-OCTOBER-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE STREET: 2000 K St., N.W., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                               1340 AGCATAACTTTGGATAAAAACAATTA 1365
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08470953A Patent No. 6346407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625
TELERA: (202) 293-1850
TELER: 650 383-5605
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 663 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 6-OCTOBER-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, E
REGISSTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                        COUNTRY: USA

ZIP: 20006-1812

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,126
FILING DATE: 29-DEC-1995
CLASSIFICATION 1425
ATTORNEY/ARENT INFORMATION:
NAME: MITSAHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET INFORMATION:
TELEPHONE: (202) 887-1500
TELEPAX: (202) 887-1501
TELEPAX: (202) 887-1501
TELEPAX: (202) 887-0763
; INPORMATION PCR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "xylanase"
                        ADDRESSEE: Morrison & Poerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CBS672.93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 95.77
Matches 714; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 1..744
CTHER INFORMATION:
US-08-501-126-18
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941 TATTTATGCGTCTATGGTTGGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGT 1000
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                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: TBM PC compatible
COMPUTER: DEADABLE
COMPUTER: DATE PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,953A
FILING DATE: 6-OCTOBER-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                             FILLING DATE:
ATORNEY AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEFAX: 650 383-5605
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 663 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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Best Local Similarity 100.
Matches 663; Conservative
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Sequence 2, Application US/08470953A

Patent No. 6346407

GENERAL INFORMATION:

APPLICANT: BRIC DE BUYL

APPLICANT: BRIC DE BUYL

APPLICANT: RENE DETROZ

TITLE OF INVENTION: Xylanase, microorganisms produced it,

TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase

TITLE OF INVENTION: and uses thereof

NUMBER OF SEQUENCES: 29

CORRESPONDENCES: 29

CORRESPONDENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE

STREET: 2000 K St., N.W., Suite 200

CITY: Washington
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                                                                                                                    0 ,
                                                                          Length 663;
                                                                                                                       Indels
                                                                Query Match
43.8%; Score 663; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 2.4e-168;
Matches 663; Conservative 0; Mismatches 0;
  Bacillus
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US-08-470-953A-1
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                                                                                                                                        TTAAGTAAATTAGTATATACTTGCGTTATCAAAATGTGAGATAATCTAATTGATCAAACA 420
                                                                   AAACCAATACTTCTTTAATTTAACGCTAACCACTTGCAATCTTATCACAAGAACATTCTTT 120
                                                                                       61 AAACCAATACTTCTTTATTTAACGCTAACCACTTGCAATCTTATCACAAGAACATTCTTT 120
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Sequence 11, Application US/09189060B

GENERAL INFORMATION:
Sequence 11, Application US/09189060B

GENERAL INFORMATION:
Sequence 12, Application US/09189060B

APPLICANT: Sandal Thomas
SAPPLICANT: Sandal Thomas
SAPPLICANT: Markus
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1 AAATTGAATTGTGTATATCTAATGATAACGACAAATCGTCACTGTTTTTAAACTAATCTC
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Pred. No. 5.6e-148;
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86.8%;
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Best Local Similarity
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; LOCATION: (1).
US-09-189-060B-11
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US-09-189-060B-11
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   GILSON & LIONE,
200
                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/275,526C
FILING DATE: 15-UUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 282.8; DB 3;
Pred. No. 3.4e-66;
); Mismatches 287;
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Suite
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                                                                                                                                                                                                                                                                               NAME: Gadiano, Wilhlem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4122
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: 650 383 5605
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1022 base pairs
                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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PRL B12
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62.1%;
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ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
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Best Local Similarity 62.1
Matches 481; Conservative
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STRANDEDNESS: single
                                      Washington
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                                                                         COUNTRY:
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                                                                                                         CCTGCAGAAATAATTCAGGCACAAATCGTCACCGACAATTCCATTGGCAACCACGATGGC
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     Gaps
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EXPRESSION VECTORS FOR SUCH XYLANASE AND
OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
USE THEREOF
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 Indels
                                    98;
 Mismatches
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Patent No. 6180382
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LEDOUX, PIERRE
AMORY, ANTOINE
DETROZ, REN
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Conservative
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APPLICANT: LAHAYE, AJ
APPLICANT: LEDOUX, P
APPLICANT: AMORY, AN
APPLICANT: AMORY, AN
APPLICANT: AMORY, R
TITLE OF INVENTION:
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US-08-275-526C-1
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VETTER, ROMAN
VETTER OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
EXPRESSION VECTORS FOR SUCH XYLANASE AND
OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K St., N.W., Sulte 200
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DETROZ, RENE
ANDRE, CHRISTOPHE
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LAHAYE, ANDREE
LEDOUX, PIERRE
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US-09-076-677-1
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      639 ACGCTCCGTGTCAATCAGCCTTCTATCATTGGAGACGCTACCTTCAAACAATATTGGAGT 698
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/275,526C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Gadiano, Wilhlem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: (202) 233-0625
ITELEFAX: (502) 233-0625
INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 35, Application US/08275526C Patent No. 6180382 GENERAL INFORMATION:
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DETROZ, REN
ANDRE, CHRISTOPHE
VETTER, ROMAN
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N: 435
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ATTORNEY/AGENT INFORMATION:
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LENGTH: 1022 base pairs
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LEDOUX, PIERRE
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Best Local Similarity
Matches 481; Conserv
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US-08-275-526C-35
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1079 ACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGT
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CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K St., N.W., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08/275,526
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APPLICATION NUMBER: US/09/076,677
FILING DATE: 12-May-1998
CLASSIFICATION: <Unknown>
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FILING DATE: 15-7UL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gadiano, Wilhlem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-49
TELECOMMUNICATION INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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TELEFAX: (202) 293-0625
TELERX: 650 343 5605
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 35, Application US/09076677
Patent No. 6423523
GENERAL INFORMATION:
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DETROZ, RENE
ANDRE, CHRISTOPHE
VETTER, ROMAN
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LAHAYE, ANDREE
LEDOUX, PIERRE
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington
STATE: D.C.
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US-09-076-677-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        342 TCGATGACACTCAATAACGGCGGGGCATTTAGTGCAAGCTGGAACAATATTGGAAATGCC 401
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                                                                                                                                                                                                                                                                                         Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:

NAME: Gadiano, Wilhlem F.

REGISTRATION NUMBER: 37,136

REFERENCE/DOCKET NUMBER: 4121-49

TELECOMMUNICATION INFORMATION:

TELEFAX: (202) 429-0625

TELEFAX: (202) 293-0625

TELEFAX: 600 383 5605

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1022 base pairs
                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,677
FILING DATE: 12-May-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/275,526
FILING DATE: 15-JUL-1994
                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANIGM: Bacillus pumilus
STRAIN: PRL B12
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                  ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: genomic DNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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CITY: Washington
                                                                            COUNTRY: U.S.A.
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                                                                                        599 AATTAAAAGGAGGAATGCCTAATGAGACAAAAGAAATTGACGTTGATTTTAGCCTTTTTA 658
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                                                                                                                                                                                                                                                                     719 TCCATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAAGATAGCGGTGGCTCTGGG 778
                                                                                                                                                                                                                                                                                                               285 AGGATAGGGACACACAGCGGATACGATTTTGAATTATGGAAGGATTAC---GGAAATACC 341
                                                                                                                                                                                                                                                                                                                                                                                                     342 TCGATGACACTCAATAACGGCGGGGCATTTAGTGCAAGCTGGAACAATATTGGAAATGCC 401
                                                                                                                                                                             659 GITHGITTHGCACTAACCTTACCAGAAATAATTCAGGCACAAATCGTCACCGACAAT
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                                              9
  Length 1022;
Score 282.8; DB 4;
Pred. No. 3.4e-66;
0; Mismatches 287;
    18.7%;
62.1%;
  Query Match
Best Local Similarity 62.1;
Matches 481; Conservative
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Search completed: November 11, 2004, 01:34:23 Job time: 176.81 secs

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November 10, 2004, 21:26:43; Search time 967.351 Seconds (without alignments) 8421.106 Million cell updates/sec
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10: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.Seq:*
11: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.Seq:*
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14: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.Seq:*
15: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.Seq:*
16: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.Seq:*
17: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.Seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3611042 seqs, 2692057975 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                       OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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1513
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description		Sequence 10, Appl	Sequence 11, Appl	Sequence 4, Appli	Sequence 5, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 12, Appl	Sequence 13, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 39, Appl	Sequence 71, Appl
SUMMARIES				US-09-909-207-10	US-09-909-207-11	US-09-909-207-4	US-09-909-207-5	US-09-909-207-1	US-09-909-207-2	US-09-909-207-12	US-09-909-207-13	US-09-770-621-1	US-10-286-993-1	US-10-307-441-39	US-10-213-990-71
		E C	ij	6	σ	σ	σ	σ	σ	σ	σ	σ	15	15	14
		Query Match Length DB		1513	1513	744	744	663	663	619	150	1375	1375	296	942
	dР	Query		100.0	100.0	49.2	49.2	43.8	43.8	40.9	6.6	7.9	7.9	7.6	7.4
		ar C) !	1513	1513	744	744	663	663	619	150	119.4	119.4	115.2	111.4
		Result		1	7	m	4	'n	9	7	8	6	10	11	12

11, 11, 64, 65,	Sequence 6, Appliance Sequence 2, Appliance 10, Appliance 11, Appliance 11, Appliance 11, Appliance 12, Appliance 12, Appliance 12, Appliance 5, Appliance 5, Appliance 6, Appliance 12, Appliance 12, Appliance 13, Appliance 13, Appliance 13, Appliance 14, Appliance 15,	8 4 10, 4 8	1, 829 371 177 9, 1, A
4 4 6 4 4 4 6	10000000000000000000000000000000000000	100 000 000 000 000 000 000 000 000 000	014 16 US-10-244-596-1 749 18 US-10-425-115-82922 818 18 US-10-425-115-37733 850 18 US-10-425-115-177283 588 15 US-10-425-116-177283 983 9 US-09-467-368-1 3778 15 US-10-312-841-2 13778 15 US-10-312-841-1 1054 15 US-10-419-969-5
7.3 1002 7.2 705 7.0 2898 6.9 712 6.8 666	55.7 678 55.6 1023 55.6 1025 55.5 645 55.5 1011 55.5 1011	5.5 1023 5.5 1023 5.4 1023 5.4 1023 5.4 1023 5.2 1023 5.2 2225	5.1 1014 5.1 749 5.0 818 4.9 850 4.8 583 4.8 983 3.8 3673778 3.7 3673778
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ALIGNMENTS

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RESULT.

US-09-107-10

Sequence 10, Application US/09909207

Sequence 10, Application US/09909207

Patenn No. US20020115181A1

GENERAL INFORMATION:

RENE DETROIL

PIERRE LEBOUX

RENE DETROIL

PIERRE LEBOUX

RENE DETROIL

TITLE OF INVENTION: Xylanase, microorganisms produced it,

DNA molecule, processes for preparation of this xylanase and uses thereof

NUMBER OF SEQUENCES: 3

CORRESPONDENCE 30

CORRESPONDENCE ADDRESS:

ADDRESSES: WILLIAN BRINKS HOPER GILSON & LIONE

STATE: 2000 K St., N.W., Suite 200

CITY: Washington

STATE: D.C.

CONPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

CONPUTER PATONIN NW. St., N.W., Suite 200

SOFTWARE: D.C.

CONPUTER PATONIN NUMBER: US/09/909, 207

FILING DATA: 9-401-2001

CLASSIFICATION NUMBER: 0470, 953

FILING DATE: OG-UUNE-1995

ATTORNEY APPLICATION NUMBER: 06-UUNE-1995

ATTORNEY/AGENT INFORMATION: ESG
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1080 1080 11140 11140 1260 1260 1320

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CATAAACTACGGGGGCCAACTTCCAACCAAATGGTAATGCGTATTTATGCGTCTATGGTTG
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CORRESPONDENCE ADDRESS:
ADDRESSE: WILLIAN BRINKS HOFER GILSON & 1
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
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Patent No. US20020115181A1
GENERAL INFORMATION:
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ERIC DE BUYL
PIERRE LEDOUX
RENE DETROZ
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  4121-40
                                                                                                                                                                                STRAIN: Bacillus
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                         TELEPHONE: 202-429-0625
TELEPAX: (202) 299-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                             LENGTH: 1513 base pairs
                                                                                                                            TOPOLGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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100.0%;
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Best Local Similarity 100.
Matches 1513; Conservative
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            GATAATTATCCAGTTTCAAAATTTGAAATAGTGTGTATGGAATAGTTTGAATGTCAACTG
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                                                        Version #1.25
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 COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/909,207
FILING DATE: 19-UNI-2001
CLASSIFICATION: <UNKNOWN>
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100.0%; Pred. No. 0;
rative 0; Mismatches
                                                                                                                             PKIOK AFFLICATION NUMBER: 08/470,953
APPLING DATE: 06-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: sig_peptide
LOCATION: 620..700
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1513 base pairs
TYPE: NUCleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: mat_peptide
LOCATION: 701..1363
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LOCATION: 620..1363
                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            STRAIN: Bacillus
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Best Local Similarity 100.
Matches 1513; Conservative
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RENE DETROZ
TITLE OF INVENTION: Xylanase, microorganisms produced it,
DNA molecule, processes for preparation of this xylanase
and uses thereof
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CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PCC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/909,207
FILING DATE: 19-U1-2001
CLASSIFICATION: <unimoderate control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contro
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FILING DATE: 06-JUNE-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ANDREE LAHAYE
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DNA molecule, processes for preparation of this xylanase
and uses thereof
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CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE
'STREET: 2000 K St., N.W., Suite 200
CITY: Washington
'STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version #1.25
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Best Local Similarity 100.0%; Pred. No. 1.3e-166;
Matches 744; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTER: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/909,207
FILING DATE: 19-011-2001
CLASSIFICATION: <Unknown>
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FILING DATE: 06-4UNE-1995
ATTONEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN: Bacillus
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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TELEFAX: (202) 299-1850
TELEX: 650 883-5605
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                          Sequence 4, Application US/09909207
Patent No. US20020115181A1
GENERAL INFORMATION:
APPLICANT: ANDREE LAHAYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                          ERIC DE BUYL
PIERRE LEDOUX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
1501 CCTCCGTCACTAG 1513
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                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF
                                                                                                                                                 US-09-909-207-4
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RENE DETROZ
TITLE OF INVENTION: Xylanase, microorganisms produced it,
DNA molecule, processes for preparation of this xylanase
and uses thereof
                                                           GTATATAGCAATACACTAAGAATTAACGGTAACCCTCTCTCAACTATTAGTAATGACGAG 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         761 GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGG 820
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                                                                                         Length 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: WILLIAMS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version #1.25
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43.8%; Score 663; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 2.3e-147;
Matches. 663; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/470,953
FILING DATE: 06-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: uS/09/909,207
FILING DATE: 19-Uul-2001
CLASSIFICATION: <u curronnom</li>
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                                                                                                                                                  1340 AGCATAACTTTGGATAAAAACAAT 1363
                                                                                                                                                                            ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
                                                                                                                                                                                                                                                                         US-09-909-207-1; Sequence 1, Application US/09909207; Patent No. US20020115181A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 663 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                           ERIC DE BUYL
PIERRE LEDOUX
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ANDREE LAHAYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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Best Local Similarity 100.0%; Pred. No. 1.3e-166;
Matches 744; Conservative 0; Mismatches 0;
                             REGISTRATION NUMBER: 37, 136
REPERENCE/DOCKET NUMBER: 4121-40
TELEPHONE: 202-429-0625
TELEPAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 1..81 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                 NAME: Wilhlem F. Gadiano, Esq.
                                                                                                                                                                          SEQUENCE CHRACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sig_peptide
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                                                                                                                                                                                                                                                                                                                          STRAIN: Bacillus
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100.0%; Pred. No. 2.3e-147;
iive 0; Mismatches 0;
                                                                NAME: Wilhlem F. Cadiano, Esq.
REGISTRATION NUMBER: 37,136
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625
TELEFAX: (502) 293-1850
TELEFAX: (502) 293-1850
TELEFAX: (503) 293-1850
TELEFAX: (503) 293-1850
TELEMORY: 663 base pairs
TYPE: Nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1..663
SEQUENCE DESCRIPTION: SEQ ID NO:
                    APPLICATION NUMBER: 08/470
FILING DATE: 06-JUNE-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: mat_peptide LOCATION: 1..663
     PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                        STRAIN: Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 663; Conservative
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DNA molecule, processes for preparation of this xylanase
and uses thereof
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CORRESPONDENCE ADDRESS:
ADDRESSE: WILLIAN BRINKS HOFER GILSON & LIONE STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/909,207
FILING DATE: 19-Jul-2001
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERIC DE BUYL
PIERRE LEDOUX
RENE DETROZ
TITLE OF INVENTION: Xylanase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09909207
Patent No. US20020115181A1
GENERAL INFORMATION:
APPLICANT: ANDREE LAHAYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 20006
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US-09-909-207-2
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QY 1301 ATTANCGGTAACCCTCTCTCAACTATTAGTAATGACGAGAGCATAACTTTGGATAAAAAC 1360 Db 601 ATTAACGGTAACCCTCTCTCAACTATTAGTAATGACGAGAGCATAACTTTGGATAAAAAC 660 QY 1361 AAT 1363 Db 661 AAT 663	Db 121 ATAGGAACTTTCCCATTTGCAAGACGATAAAATCTTTTCCCCTATTTTATCTTATCG 180 Qy 181 CCTTGATCGGTTTAATTTGTAAACTTTATTTTAGTTTACGTGATGTTCCTCATTCAT
RESULT 7 US-09-909-207-12 ; Sequence 12, Application US/09909207 ; Patent No. US20020115181A1 ; GENERAL INFORMATION: ; APPLICANT: ANDREE LAHAYE	OY 301 ATTANGTCATATTTCTCACGCCGCTCCATAATGGAATATATATAT
FERRE LEDOUX FERRE LEDOUX FRENE DETROZ TITLE OF INVENTION: Xylanase, microorganisms produced it, DAM molecule, processes for preparation of this xylanase and uses thereof	Db 361 TIAAGTAATTAGTATATACTTGCGTTATCAAAATGTGAGATAATCTAATTGATCAAAAC 420 Qy 421 AGCAGCTATCCCAAAAACACTGATGTTGACCTCTTAAAGAAGTGTCACTATGAAAA 480 Db 421 AGCAGCTATCCAAAAAACACTGATGTTGACCTCTTAAAGAAGTGTCACTATGAAAA 480
ACES: ADDRE WILI 00 K	Oy 481 GATAATTATCCAĞITTCAAAATTGAAATAGTGTGTATGGAATAGTTTGAATGCTCAACTG 540
	541
CMPUTER: FLOREY CLSA COPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25	601
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/909,207 FILING DATE: 19-Jul-2001, CLASSIFICATION: CURKNOWN: PRIOR APPLICATION DATA: CLASSIFICATION: CONTROL OF THE	RESULT 8 US-09-909-207-13 ; Sequence 13, Application US/0990207 ; Patent No. US20020115181A1 ; GENERAL INFORMATION:
APLICATION NUMBER: 06-JUNE-1995 FILING DATE: 06-JUNE-1995 ATTORNEY/ACENT INFORMATION: NAME: Wilhlem F. Gadiano, Esq. REGISTRATION NUMBER: 37,136	e, microorganisms produced it,
TELECHMUNICATION INFORMATION: TELEPHONE: 202-429-0625 TELEPAX: (202) 293-1850 TELEFAX: (502) 293-1850 INFORMATION FOR SEQ ID NO: 12:	DNA molecule, processes for preparation of this xylanase and uses thereof CORRESPONDENCES: 29 CORRESPONDENCE ADDRESSE: WILLIAM BRINKS HOFER GILSON & LIONE CORRESPONDENCE WILLIAM BRINKS HOFER GILSON & LIONE CORRESPONDENCE WILLIAM BRINKS HOFER GILSON & LIONE
SEQUENCE CHARACTERISTICS: LENGTH: 619 base pairs TYPE: nucleic acid STRANDEDNESS: single MOLECTURE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 12:	SINGEL: 2000 N.S., N.M., SECONO SINGER SINGE
US-09-909-207-12 Query Match Best Local Similarity 100.0%; Pred. No. 6.5e-137; Matches 619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CURREATING SYSTEM: PC-DOS/MS-DOS CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/909,207 FILING DATE: 19-Jul -2001
Qy 1 AAATTGAATTGTGTATATCTAATGATAACGACAAATCGTCACTGTTTTTAAACTAATCTC 60	CLASSIFICATION: <unknown> PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/470,953 FILING DATE: 06-UINE-1995</unknown>
Qy 61 AAACCAATACTTGTTTAACGCTAACCACTTGCAATCTTATCACAAGAACATTCTTT 120	ATORNEY/AGENT INFORMATION: NAME: Wilhlem F. Gadiano, Esq. REGISTRATION NUMBER: 37,136 REFERENCE/DOCKET NUMBER: 4121-40
OY 121 ATAGGAACTITCCCATTIGCAAGACGATAAAAATCTITITCCCCTATITTATCTTATC	TELECOMMUNICATION INFORMATION: ; TELEPHONE: 202-429-0625

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Conservative
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Matches 238; Conserv
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LOCATION:
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Patent No. US20010024815A1
FEBREAL INFORMATION:
APPLICANT: Whith Aria
APPLICANT: Vehmanper, Jari
APPLICANT: Lantto, Raila
APPLICANT: Lantto, Raila
APPLICANT: Lantto, Maria
APPLICANT: Lantto, Maria
APPLICANT: Lantto, Maria
APPLICANT: Lantinen, Pirkko
APPLICANT: Lantinen, Pirkko
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                                                                                                                                                                                                                                                                                                                                            Length 150;
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MEDLUM TYPE: Floppy disk
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CONFUTER: BATENING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: DATA:
APPLICATION: DATA:
APPLICATION: DATA:
APPLICATION: DATA:
APPLICATION: DATA:
APPLICATION: NUMBER: 08/590,563
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                                                                                                                                                                                                                                                                                                                                       Query Match 9.9%; Score 150; DE Best Local Similarity 100.0%; Pred. No. 1.3 Matches 150; Conservative 0; Mismatches
                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
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FILING DATE: 29-JUL-1994
CLASSIFICATION:
TTORNEY AGENT INFORMATION:
NAME: Bugaisky, Lawrence B.
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                           LENGTH: 150 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                  US-09-909-207-13
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APPLICANT: Suominen, Pirkko
APPLICANT: Suominen, Pirkko
APPLICANT: Suominen, Pirkko
APPLICANT: Vehmaanpera, Jari
TITLE OF INVENTION: Production and Secretion of Proteins in Filamentous
TITLE OF INVENTION: Fungi
FILE REFERENCE: 1716.034004
CURRENT APPLICATION NUMBER: US/10/286,993
FILE REFERENCE: 1716.034004
PRIOR APPLICATION NUMBER: US/09/120,804
PRIOR APPLICATION NUMBER: PCT/F197/00037
PRIOR PILING DATE: 1998-07-23
PRIOR PILING DATE: 1996-01-24
PRIOR FILING DATE: 1996-01-26
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57.1%; Pred. No. 7.1e-18;
iive 0; Mismatches 176;
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 Beap pairs
TYPE: nucleic acid
STRANDENNESS: No. US20010024815A1 Relevant
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APPLICANT: Paloheimo, Marja
APPLICANT: Lantto, Raija
APPLICANT: Fagerstrom, Richard
APPLICANT: Lahtinen, Tarja
APPLICANT: Suominen, Pirkko
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MOLECULE TYPE: DNA (genomic)
FEATURE:
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3,

Mismatches 163; Indels

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Matches 226; Conservative
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APPLICANT: SING, Wing L.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
TITLE OF INVENTION: and Alkalophilicity
FILE REPERENCE: 027367-5006US
CURRENT APPLICATION NUMBER: US/10/307,441
CURRENT PILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: PCT/CA01/00769
PRIOR FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 60/213,803
PRIOR FILING DATE: 2000-05-31
SUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
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US-10-307-441-39
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Pred. No. 7.1e-18;
0; Mismatches 176;
                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Actinomadura flexuosa (Strain: DSM43186)
                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (303)..(1337)
; OTHER INFORMATION: Product= AM35 xylanase
US-10-286-993-1
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ORGANISM: Artificial Sequence
                                                                          3.0
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Best Local Similarity 57.1%;
Matches 238; Conservative
               NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version
SEQ ID NO 1
                                                                                                                                                                              LENGTH: 1375
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Score 115.2; DB 15; Length 596; Pred. No. 4.7e-17;

7.68;

Best Local Similarity

Query Match

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APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
TITLE OF INVENTION: BUSTMES AND METHODS OF USE
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT PILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                      1070 ATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATTAAACAA 1129
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                                                                                311 AATCCGAGTACCGGCGCACAAATTAGGCGAAGTCACTAGTGATGGATCGGTATATGAT 370
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                     250
                                                                                                                                     251 TATGGCTGGTCTAGAAGCCCACTGATTGAATATTACATTGTCGAAAATTTCGGTACCTAC 310
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191 MATAAGGIGATCATCATGTGTCTTATAATCCGAATGGGAATTCATACTTAAGGGTC
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57.0%; Pred. No. 4.7e-16;
tive 0; Mismatches 166;
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Publication No US20030082595A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Bussey, Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 57.0
Matches 224; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Aspergillus
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; LOCATION: (1)
US-10-213-990-71
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US-10-213-990-71
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7.2%;
ilarity 51.9%;
Conservative 0
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Matches 298; Conserv
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US-10-213-990-68
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US-10-299-393-1
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Sequence 70, Application US/10213990
Publication No. US200300825951
Sequence 70, Application No. US200300825951
APPLICANT: Stang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Scorms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: BUSY, BOUCHERC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
TITLE OF INVENTION: BUSY, BOUCHERC ACIDS OF USE
FILE REFERENCE: 10.182-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT PILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
                                                         CATITIAAACAATATIGGAGTGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCA 1178
                                                                                                                               1179 GCAACCACTTTAGAGCGTGGGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCG 1238
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                                                                                                                                                                 557 CGAATCACTTCAAGGCCTGGGCTAGTCTGGGGTGAACCTGGGTACCCATAACTATCAGA 616
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396 GACTACCAACCCCTAGTCGAATACTACATCCTCGAGAACTATGGCAGTTACAATCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     456 CTCGGGCATGACGCACAAGGGCACCGTCACCAGCGATGGATCCACCTACGACATCTATGA
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                                                                                           497 corrcaaccaaracregrecarececeaaacaagearecagegeacagegeacaceg
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Pred. No. 1e-15;
0; Mismatches 155; Indels
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                                                                                                                                                                                                                                        617 TTGTTTCCACTGAGGATATGAGAGCAGCGGTA 649
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Best Local Similarity 57.8%;
Matches 216; Conservative
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; ORGANISM: Aspergillus
US-10-213-990-70
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LENGTH: 1002
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RESULT 14 US-10-213-990-68

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Sequence 68, Application US/10213990

Publication No. US20030082595A1

GENERAL INFORMATION:

APPLICANT: Jiang, Bo

APPLICANT: Storms, Reg

APPLICANT: Storms, Reg

APPLICANT: Storms, Reg

TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL

TITLE OF INVENTION: NUMBER: US/10/213,990

CURRENT APPLICATION NUMBER: US/10/213,990

CURRENT FILING DATE: 2002-08-05

NUMBER OF SEQ ID NOS: 72

SEQ ID NO 68

LENGTH: 705
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Pred. No. 1.7e-15;
0; Mismatches 267; Indels 9;
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; Publication No. US20030108642A1
; GENERAL INFORMATION:
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  APPLICANT: Fish, Neville Marshall
APPLICANT: Haigh, Neville Marshall
APPLICANT: Haigh, Nigel Paterson
TITLE OF INVENTION: PENICILIUM FUNICULOSUM STRAIN USEFUL.
TITLE OF INVENTION: FOR THE PRODUCTION OF ENZYMES
FILE REFERENCE: A32917-PCT-USA-I (072667.0183)
CURRENT APPLICATION NUMBER: US/10/299,393
CURRENT APPLICATION NUMBER: 2002-11-19
PRIOR APPLICATION NUMBER: 2006-04-07
PRIOR FILING DATE: 2006-04-07
PRIOR FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO : LENGTH: 2898
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Best Local Similarity 56.54
Matches 218; Conservative
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LOCATION: (1644)...(2042)
FEATURE:
NAME/KEY: RBS
LOCATION: (570)...(576)
APPLICANT: Sabatier, Alain
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LOCATION: (1590)...(1642)
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LOCATION: (1317)...(1589)
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; LOCATION: (724)...(730)
US-10-299-393-1
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Search completed: November 11, 2004, 02:08:28 Job time : 972.351 secs

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C C 25.5	308				4 4 4 4 3			RESULT 1 CF472462 LOCUS	DEFINITION	ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AITHORS	TITLE	JOURNAL	ř	FEATURES SOURCE		
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: November 10, 2004, 16:24:32; Search time 6558.71 Seconds (without alignments) 8406.125 Million cell updates/sec	Title: US-09-909-207-10 Perfect score: 1513 Sequence: 1 AAATTGATATATCTTGAAACACCTCCGTCACTAG 1513	Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0	Searched: 32822875 segs, 18219865908 residues	Total number of hits satisfying chosen parameters: 65645750	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries	ĒΛ	1: 9b est1:* 2: 9b est2:* 3: 9b htc:* 4: 9b est3:* 5: 9b est4:* 6: 9b est5:* 9: 9b gss1:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	ore M	1 98.6 6.5 618 7 CP472462 CF472462 RTDSL_9C 2 93 6.1 728 7 CN132941 CN133042 CN133042 CN133042 4 91.8 6.1 724 7 CR133042 CR867983 CR8679978 CR8679781 CR8679781 CR8679781 CR8679781 CR867978 CR867978 CR867773 CR867773 CR867978 CR867773 CR867773 CR867978 CR867773 CR867978 CR867773 CR867773 CR867978 CR867773 CR867978 CR867773 CR867978 CR867773 CR867773 CR867978 CR867773 CR867978 CR867773 CR867978 CR867773 CR867773 CR867978 CR867773 CR8677773	9 CNSOOBVL ALO69706 5 BQ471960 CD464005 6 CNSOO21J ALO61936 6 BY720774 ALO61936 6 BY720774 ALO61936 9 CNSOOBVL BO66459706 9 CNSOOBVL BO664591 9 CNSOODD1 CC263147 9 CNSOODD1 CC263147 9 CNSOODD1 CC263147 9 CNSOOCCP ALO65919 9 CNSOOCCP ALO65919 9 CNSOOCCP ALO69440 9 CNSOOCC ALO69440 9 CNSOOCC ALO69440 9 CNSOOCC ALO69440 9 CNSOOCC ALO69440 9 CNSOOCC ALO69440 9 CNSOOCC ALO69440 9 CNSOOCC ALO69440 9 CNSOOCC ALO69440 9 CNSOOCC ALO69440 9 CNSOOCC ALO69440	ALIGNMENTS CF472462 CF472462 CFA72462 CFA72462 CFA72462 CF472462 CF472462 CF472462 CF472462 CF472462 CF472462 CF472462.
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Cordonnier Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Lim, S., Eastman, A. and Pratt, L.H.
An EST database from Sorghum: oxidatively stressed leaves and roots Other ESTs: OX1 9 D10.91 A002
Contact: Cordonnier-Pratt MM
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fax: 706 583 0210
ramet clones until predawn needle water potential re-1.75 MPa. On day 7 roots were harvested for RNA insolation. Double-extranded cDNA was cloned unidirectionally into pS11180. Inserts excised with (5' end) and XhoI (3' end)."
                                                                                                                                                                                                                      3;
                                                                                                                                                                   / Match 6.5%; Score 98.6; DB 7; Length 618; Local Similarity 57.4%; Pred. No. 2.8e-12; nes 198; Conservative 0; Mismatches 144; Indels
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POLYA=Yes.
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Sorghum bicolor
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/db xref="taxon:4558"
/db xref="taxon:4558"
/lab host="mild="This phage-resistant E. coli"
/lab host="mild=This phage-resistant E. coli"
/clone lib="Oxidatively-stressed leaves and roots"
/clone lib="Oxidatively-stressed leaves and roots"
/note="Organ: Leaf and Root; Vector: pME18S-FL3; Site_1:
Xhoi; Site_2: Xhoi; The library was prepared from polyA+RNA from oxidatively stressed, hydroponically grown sorghum seedlings. At 8 days of age, growth medium was supplemented with hydrogen peroxide to 0.003% and leaves were misted with 10 um methyl viologen. Leaves and roots were harvested at 3, 12 and 27 hr after treatment and all tissue pooled bouble-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACTGTGTG). Thoi excises the cDNA insert."
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Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Lim, S., Eastman, A. and Pratt, L.H.

An EST database from Sorghum: oxidatively stressed leaves and roots Unpublished (2003)
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OX1_9_D10.g1_A002 Oxidatively-stressed leaves and roots Sorghum bicolor cDNA_clone OX1_9_D10_A002 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 CCATCAACTATGGCGGTTCTTTCAGCCCTCAGGGTAACGGCTACCTCTGCGTCTACGGCT
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Pred. No. 5.8e-11;
0; Mismatches 180; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCAGAGCAGTGGATCTTCTATCTATGTCCAGAC 497
organism="Sorghum bicolor"
                                    /mol_type="mRNA"
/cultivar="BTx623"
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                                                           CF867983 1-OCT-2003 tricol3xe09.bl T.reesei mycelial culture, Version 6 October 2003 Hypocrea jecorina cDNA clone tricol3xe09, mRNA sequence.
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in a comprehensive set of expressed sequence tags from Trichoderma
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/clone_lib="T.reesei mycelial culture, Version 6 October
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Diener, S. B., Dunn-Coleman, N., Foreman, P., Houfek, T.D.,
Teunissen, P.J.M., van Solingen, P., Dankmeyer, L., Mitchell, T.K.,
Ward, M. and Dean, R.A.
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Hypocreomycetidae, Hypocreales; Hypocreaceae; Hypocrea
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55.0%; Pred. No. 1.1e-10;
tive 0; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                                                            Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lett. 230 (2), 275-282 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEMS Microbiol. Lett. 230 (2), 275-282
Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
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/mol_type="mRNA"
/strain="QM6a"
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/clone="tric013xe09"
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Email: ralph dean@ncsu.edu
Seg primer: LT-Fl primer.
Location/Qualifiers
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/clone="OX1 9 D10 A002"
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/note="Oxidatively stressed, hydroponically grown sorghum seedlings. At 8 days of age, growth medium was supplemented with hydrogen peroxide to 0.003% and leaves were misted with 10 um methyl viologen. Leaves and roots were harvested at 3, 12 and 27 hr after treatment and all tissue pooled. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pWE18S-FL3 vector (5-prime DraIII site is CACTGGTG, 3-prime DraIII site is CACTGGTG). XhoI excises the cDNA insert."
                                                                                                                                                                                                                                                                                                                    Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University,
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
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                                                                               Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fal: 706 542 1860
Fax: 706 583 0210
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Location/Qualifiers
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Other ESTs: OX1 9 D10.bl A002
Contact: Cordonnier-Pratt MM
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Tel: 706 542 1860
Fax: 706 583 0210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db.cref="texcon:51453"
/clone="tric013xe09"
/dev stage="mycelia"
/clone lib="T.reessi mycelial culture, Version 3 april"
/note="Vector: pREP3Y; Site 1: Not I/Sal 1; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."
                                                                                                                                                                                                                      Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (bases 1 to 799)
Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,
Dunn-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G.J.,
Kelley, A.S., Meerman, H.J., Yao, J., and Ward, M.
Transcriptional regulation of biomass-degrading enzymes in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  893 AACATGTCCATAAACTACGGAGCCAACTTCCAACCAAATGGTAATGCGTATTTATGCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         528 AACCCGTCCACGGGCGCCACCAAGCTGGGCGAGGTCACCTCCGACGGCAGCGTCTACGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  925 Page Mill Road, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'organism="Hypocrea jecorina"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Pforeman@genencor.com
Seg primer: LT-F1 primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Pamela K. Foreman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="QM6a"
                                                                                                                                                                             CB898036.1 GI:30112694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: (650) 846-7635
Fax: (650) 621-7817
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Best Local Similarity
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SOURCE
ORGANISM
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MEDLINE
PUBMED
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                                           RESULT 5
CB898036
                                                                                                                                                                                                                                                                                                                       REFERENCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Cade; Portain District Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD cade; Panicoideae; Andropogoneae; Sorghum.

1 (Dases 1 to 738)

2 Cordonnier-Pratt, M.-M., Wentzel, V., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Shah, M., Salzman, R., Chua Tan, N., Gonzalez, M., Lane, S., Miller, V., Nanda, P., Olaseinde, O., Bastman, A. and Pratt, L.H.

An EST database from Sorghum: 1-aminocyclopropane-1-carboxylic acid (ACC)-treated seedlings

Unpublished (2003)

Other_ESTS: ETH1 48_B06.bl A002

Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bloinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
CD464145
ETH1_48_B06.gl_A002_Ethylene-treated seedlings Sorghum bicolor CDNA clone ETH1_48_B06_A002_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & W University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below bred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
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/note="Vector: pME188-FL3; Site_1: Xho1; Site_2: Xho1; The library was prepared from polyA+ RNA from seedlings grown in hydroponic culture. At 8 days of age, medium was supplemented with 0.5 mM 1-aminocyclopropane-1-carboxylic acid (ACC) to induce endogenous ethylene (ETH) production. Roots and shoots were harvested after 27 and 72 hr and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  material from both time points was combined prior to RNA isolation. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3-prime DraIII site is CACCATGTG). XhoI excises the cDNA
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/c1one="ETH1 48 B06_A002"
/lab_host="DH10B-T1_phage-resistant E. coli"
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Pred. No. 1.8e-09;
0; Mismatches 174; Indels
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Location/Qualifiers
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/mol_type="mRNA"
/cultivar="BTx623"
                                                                                                                                                                                                                                                            Sorghum bicolor (sorghum)
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52.48;
                               208; Conservative
   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Fg08_AAFC_ECORC_Fusarium_graminearum_complex_s
                                                                                                                                                                                                     1076
                                                                                                                                                                                                                                                                                                                                      1077 AGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATTTAAACAATATTGGA 1136
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                                                                        960 GGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGTTGGGGCAACTGGCGTCCAC 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        644
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      345 CCATCAAGTACTCTGGTACTTACAACATCAACGGAAACAGCTACCTCGCTGTTTACGGAT 404
                                                                                                                                                                                                         1020 CA---GGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGAACATATGATATCTACG
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Gibberella zeae
Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes;
                                                                                                                                                                                                                                                             CTTCCGGCGCCAGAAGAAGAGGTGAGGTCACTGTTGACGGATCTGTCTACGACATCTACG
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                                                                                                                                       405 GGACTCAGAACCCTCTCATCGAGTACTACATCGTTGAGAACTTCGGCACCTACAACCCT
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Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 20, Central Experimental Farm, Ottawa, Ontario, KlA OC6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

(bases 1 to 921)
Watson, R.J., Heys, R., Chapados, J., Couroux, P., Harris, L.J.,
Hattori, J., Lacroix, C. Ouellet, T., Robert, L.S., Singh, J.A.,
Sprott, D. and Tinker, N.A.
A cDNA library prepared from Fusarium graminearum grown on a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'organism="Gibberella zeae"
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/clone="Fg08 04b10"
/tissue_type="Mycelium"
/dev atage="Asexual"
/lab_host="E. coli DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="DAOM 180378"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pax: (613) /5y-.v.
Email: watsonrj@agr.gc.ca.
Location/Qualifiers
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DEFINITION
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AUTHORS
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KEYWORDS
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Length 921;

DB 6;

5.5%; Score 83.4;

Query Match

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/tissue type="protoplasts"
/lab hogt="E. coli DH10B"
/clone lbh="CUGI Rice Blast BAC Library"
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devestating fungal diseases
of rice world wide. It is a filamentous ascomycete with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ160513 603 bp DNA linear GSS 09-SEP-1998 mgxb0006621r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
                                                                                                                                                                                                                                                                                                              1076
                                                                                                                                                                                            GGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGTTGGGGGCAACTGGCGTCCAC 1019
                          ä
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                                                                                                                                   422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Sasinowski, M. Wing, R.A. and Dean, R.A. A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                 483 gcadccaeddrcadcaccaadaradccricracaccdacddrdacadcracdarara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1197 GGGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCGCTTACTGTAGAAGGCT
                                                                                                                                                                                                                                                  423 deaccecedereceretedreficadaracriacareareaserracaeeeee
                                                                                                                                                                                                                                                                                                              1020 CAGGA---GCAACGCCTAAGGGGACCATCACTGTTGATGGAGGAACATATGATATCTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1137 GIGITCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGCAACCACTTTAGAGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
                                                                                                                                      363 ccarcaacracedaeerrccrrcaacccrcaeeeraacegaraccrrrecerrraceear
                                                                                CCATAAACTACGGAGCCAACTTCCAACCAAATGGTAATGCGTATTTATGCGTCTATGGTT
                          Gaps
                          3;
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100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1257 ATCAAAGTAGCGGAAGTGCTAATGTATATAGCAATAC 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone mgxb0006C21r, genomic survey sequence
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Pred. No. 1.1e-08;
); Mismatches 186;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Dean RA
Clemson University Genomics Institute
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/mol_type="genomic DNA"
/strain="70-15"
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/clone="mgxb0006C21r"
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Location/Qualifiers
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Class: BAC ends
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임 ò 셤 ò 음 ò g ò 셤 8 g ò g ઠ g

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a haploid genome (n=7) of approximately 40 Mpp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTGTCGAATATTATATTGTCGACAGTTGGGGCAACTGGCGTCCACCA---GGAGCAACG 1030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           444 AAGAAAAAAAAAGAGACTACCAACAACAACAACAAAAAACAGCCGCGTCATCAACTACTCG 385
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Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Tel: 864 656 5737
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 82.8; DB 8; Length 6 Pred. No. 1.4e-08; 0; Mismatches 197; Indels
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Clemson University Genomics Institute
Clemson University
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AQ447125.1 GI:4576262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch 5.5%;
al Similarity 52.8%;
227; Conservative
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/tissue_types_Portoplasts"
/tissue_types_Portoplasts"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   961 GACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGTTGGGGCAACTGGCGTCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  337 GACGCGCAACCCGCTGATCGAGTACTACGTGGTGGAGAGCTTTGGCAGCTACAACCCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 TGTTCGAAGATCGAAACGCACGAGGGCACGATTTCTGTCAGCAACCACTTTAGAGCGTG
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Magnaporthe grisea
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.

1 (bases 1 to 720)
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Sasinowski, M. Wing, R.A. and Dean, R.A.
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                                                                                               grisea"
                                                                                                                                                                 /db_xref="taxon:148305"
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Class: BAC ends
High quality sequence stop: 263.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTATCAAAGTAGCGGAAGTGCTA 1277
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Best Local 9
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/lab_host="Rs. coli DH108"
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/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
/note="Vector: parameter of the most devestating thogal baseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=") of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of
kbp was constructed. This library represents greater
than 25x genome coverage. High density colony filters
are available upon request."
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                                                           AQ160254 100GI Rice Blast BAC Library Magnaporthe grisea genomic
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Y.Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M. Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
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                                                                                                                                                                                                                                                                                                          Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Bukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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larity 54.1%; Pred. No. 2e-08;
Conservative 0; Mismatches 189; Indels
                                                                                                                           clone mgxb0003L19r, genomic survey sequence.
AQ160254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db xref="taxon:148305"
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                                                                                                                                                                                                                                      GI:3557243
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Pred. No. 2e-08;
0; Mismatches 189; Indels 11;
                                                                                                                   Contact: Dean RA Contact: Dean RA Contact: Dean RA Clemson University Genomics Institute Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson University, Clemson, SC 29634 Tel: 864 656 5737
Fax: 864 656 5737
Fax: 864 656 4595
Email: rdeanGeclemson.edu
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Class: BAC ends
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                                                                  1145 AGATCGAAACGCACGAGTGGCACGATTTCTGTCAGCAACCACTTTAGAGCGTGGGAAAAC 1204
210 CGCTACAACCAGCCCTCCATCGACGCCACCAAGACCTTTCAGCAGTTCTGGTCGGTGGCG 151
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Y.Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M. Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                  150 cécaacaagcececcaécesecercaecrireceaaccaecaacecereseceaae
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Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
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848 AAAGGTAAAAATTCAATGAAACACAAAACCACCAACAAGTTGGTAACATGTCCATAAAC 907

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Query Match 5.4%; Score 81.6; DB 8; Length 786; Best Local Similarity 54.1%; Pred. No. 2.8e-08; Matches 236; Conservative 0; Mismatches 189; Indels 11;

Gaps

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את 583 bp DNA linear GSS 06-MAR-1999
mgxb0001B24f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
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TACGGAGCCAACTTCCAACCAAATGGTAATGCGTATTTATGCGTCTATGGTTGGACTGTT 967
                                                445 TACTCGGCCAGCTACAGCCCCCAGGGCAACTCATACCTGGCCGTCTACGGCTGGACGCGC 386
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Yu, Y., Zhu,H., Boyd.C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M. Wing,R.A. and Dean,R.A.
                                                                                                                                 385 AACCCGCTGATCGAGTACTACGTGGTGGAGAGCTTTGGCAGCTACAACCGTCGTCGGGC
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100 Vordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
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Magnaporthe grisea
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Clemson University Genomics Institute
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Seg primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 411.
Location/Qualifiers
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Magnaporthe grisea
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Direct Submission

Submitted (102-JUN-1999) Genoscope - Centre National de Sequencage :

Submitted (102-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster agenome using these BACs. For further information please see http://www.frutfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isoqenic strain y2; cn bw sp, the same strain used for the BDGP's
blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25% genome coverage. High density colony filters are available upon request."
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Neopiera; Endopierygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Similarity 52.8%; Pred. No. 2.9e-08;
10; Conservative 0; Mismatches 172. T.3.
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561 bp DNA linear GSS 06-NAR-1999 mgxb0010M14f CUGI Rice Blast BAC Library Magnaporthe grisea genomic AQ396475
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EST libraries. A more detailed description of the library
                                                                                                                                                                                                                                                                                                                                                                          312 ATTITCICACGCCCCCATAATGGAATATATATATCTCTTTTATACATATTAAGTAAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                546 AAAGGAGGGTAGTACCGTAGACTTCATTACCAAAATTAGTTGTAAAAATTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               918 АТАТААМААТТАТТТААТАТТТАААТАААТТТТИТТТТАТТТИТТТТИТТТТАТТТТ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTATATATCTTGCGTTATCAAAATGTGAGATAATCTAATTGATCAAACAAGCAGCTATCC
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                                                                                                                                                                                                                                                                                                                                                    72 TCTTTATTTAACGCTAACCACTTGCAATCTTATCACAAGAACATTCTTTATAGGAACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1037 ATWATTAATATWATTTTTAAAAAAAAAWTWATTTTTAATTWAAATWTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252 GITAACGCTAGAGTCATCTTTTTCGGTTCTCAAAAATACCTGAAGAACATTTATGTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                 132 CCCATTTGCAAGACGATAAAAATCTTTTCCCCTATTTTATCTTATCGCCTTGATCGGT
                  and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can found at http://bacpac.med.buffalo.edu/drosophila_bac.htm. Location/Qualifiers
                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                         Length 1101;
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                                                                                                                    melanogaster"
                                                                                                                                                                                                                                                                           Score 79.8; DB 9;
Pred. No. 7.6e-08;
                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                              /organism="Drosophila mel
/mol_type="genomic_DNA"
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/clone="tb="RRCI-98"
/note="end : T7"
                                                                                                                                                                                                                                                                                                               75;
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Matches 239; Conservative
    and
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/clone lib="Cutor Rice Blast BAC Library"
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/clone lib="Cutor Rice Blast BAC Library"
/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devestating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction.
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGTTGGGGCAACTGGCGTCCA 1018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      436 -- carcaactracagecageracagececeaggeaactraracagecegecereracagec 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 grcagcacccocracaaccacccrccarcaacaccacacaacaccrrrragecarraged 199
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                                                       1 (bases 1 to 561)
Y.Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               495 TTTTCCCanahahadgaaaaaaaaactancahcaacaacaaaaaacagccgcgr-
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Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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                                                                                                                                                                                              Unpublished (1998)
Contact: Dean RA
Contact: Dean RA
Contact: Dean RA
Contact: Dean RA
Contact: Dean RA
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 664 656 4733
Fax: 864 656 4733
Fax: 864 656 4733
Fax: 864 by 4233
Email: rdean@clemson.edu
Seq primar: TAMTACGACTCACTATAGGG
Class: BAC ende
High quality sequence start: 50
High quality sequence stap: 443.
Location/Qualifiers
1. .561
// organism="Magnaporthe grisea"
// organism="Magnaporthe grisea"
// organism="Magnaporthe grisea"
// strain="70-15"
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al Similarity 53.7%; Pred. No. 3.9e-07;
204; Conservative 0; Mismatches 170; Indels (
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Search completed: November 11, 2004, 01:16:52 Job time : 6561.71 secs

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BX324185 Danio rer
ALI33166 Human chr
Continuation (2 of
Continuation (3 of
ALIS9167 Human DNA
AC098158 Rattus no
AC137382 Rattus no
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ALI55083 Human DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unidentified unidentified unidentified unclassified.

1 (bases 1 to 185)

De, B.E., Lahaya, A., Ledoux, P., Amory, A., Detroz, R., Andre, C. and Vetter, R.

Xylanase derived from a bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC005345
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SOLVAY (BE)
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| ob_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
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28 from Patent EP0634490.
                            AC098193_6
AC098192_1
AC098192_2
AL589167_2
AL589158
AC098158
AC137382
CR383671
AC11688
AC11688
AC136569
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CNSOLDG1
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AL450308
AL450308
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A42278.1 GI:2297766
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                20.1 105587
20.0 108566
20.0 110000
20.0 120255
20.0 244759
20.0 253645
19.5 21367
19.5 233607
19.4 7218
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19.2 238007
19.1 246818
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AR220053 Sequence
AR221306 Sequence
AR221336 Sequence
AR321378 Sequence
BX000477 Zebrafish
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AR193071 Sequence
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                                                                                             November 10, 2004, 15:57:32 ; Search time 894.922 Seconds (without alignments) 9775.823 Million cell updates/sec
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1 TCATGTAACTCGCCTTGATC......AAAAAGGAGAGGGATGGAAA 185
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Compugen Ltd.
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1 (bases 1 to 185)
De Buyl, E., Lahaye, A., Ledoux, P., Amory, A., Detroz, R., Andre, C. and Vetter, R.
Xylanase derived from a bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use
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De Buyl,E., Lahaye,A., Ledoux,P. and Detroz,R.
Xylanase, microorganisms producing it, DNA molecules, methods for preparing this xylanase and uses of the latter
Patent: US 6346407-A 26 12-FEB-2002;
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tive 0; Mismatches 0;
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100.0%; Pred. No. 2.2e-45;
Live 0; Mismatches 0;
                                                                                                        Patent: US 6180382-A 28 30-JAN-2001;
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/organism="unknown"
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1 (bases 1 to 185)
S. De, B.E., Lahaye, A., Ledoux, P. and Detroz, R.
Xylanase, microorganisms for its production, DNA molecules, process of preparation and use thereof
L. Patent: EP 069867-A 26 28-FEB-1996;
SOLVAY (BE)
Other publication BE 1008751 960702
Other publication BE 1008759 960604
Other publication BE 9503454 960305
Other publication TP 8092284 960409
Other publication CA 2154628 960127
Other publication AD 2508659 960208.
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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PAT 20-APR-2002

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de Buyl, E., Lahaye, A., Ledoux, P., Amory, A., Detroz, R., Andre, C. and Vetter, R.
Xylanase derived from a bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use thereof
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Best Local Similarity 100.0%; Pred. No. 2.2e-45;
Matches 185; Conservative 0; Mismatches 0;
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Location/Qualifiers
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Sequence 28 from patent US 6426211.
AR221330. GI:23328305
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Sequence 28 from patent US 6423523.
AR220047
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1. .185
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                                                                                                                                        Bacillus pumilus
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
1 (Dases 1 to 1022)
De,B.E., Lahaya,A., Ledoux,P., Amory,A., Detroz,R., Andre,C. and Yetter,R.
Xylanase derived from a bacillus species, expression vectors for euch xylanase and other proteins, host organisms therefor and use
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Best Local Similarity 100.0%; Pred. No. 1.9e-45;
Matches 185; Conservative 0; Mismatches 0;
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1. 1022
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Other publication BR 9402834 950613
Other publication JP 7067637 950314
Other publication RI 943389 950116
Other publication CA 2128050 950116
Other publication NO 942652 950116
Other publication AU 6743294 950127
Other publication GB 2279955 950118.
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SOLVAY (BE)
  A42251 1022 bp
Sequence 1 from Patent BP0634490.
A42251
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De Buyl,E., Lahaye,A., Ledoux,P., Amory,A., Detroz,R., Andre,C. and
Vetter,R.
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De,B.E., Lahaya,A., Ledoux,P., Amory,A., Detroz,R., Andre,C. and Vetter,R.
Yalanase derived from a bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use thereof
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Other publication BR 9402834 950613
Other publication DF 7667637 950314
Other publication RI 943389 950116
Other publication CA 2128050 950116
Other publication NO 942652 950116
Other publication GB 2279955 950118.
Location/Qualifiers
                                                                                                                                                                         Patent: EP 0634490-A 35 18-JAN-1995;
SOLVAY (BE)
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Location/Qualifiers
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Sequence 1 from patent US 6180382.
AR127019
AR127019.1 GI:14113612
 1022 bp
35 from Patent EP0634490.
                                     A42285.1 GI:2297772
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Best Local Similarity 100.
Matches 185; Conservative
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1 (bases 1 to 1022) De Buyl, E., Lahaye, A., Ledoux, P., Amory, A., Detroz, R., Andre, C. and
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Best Local Similarity 100.0%; Pred. No. 1.9e-45;
Matches 185; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.9e-45;
Matches 185; Conservative 0; Mismatches 0;
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Location/Qualifiers
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(Dasse 1 to 1022) de Buyl, E., Lahaye, A., Ledoux, P., Amory, A., Detroz, R., Andre, C. and Vetter, R. Xylanase derived from a Bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use
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de Buyl,E., Lahaye,A., Ledoux,P., Amory,A., Detroz,R., Andre,C. and
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Best Local Similarity 100.0%; Pred. No. 1.9e-45;
Matches 185; Conservative 0; Mismatches 0; Indels
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Location/Qualifiers
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Sequence 1 from patent US 6426211.
AR221306
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Location/Qualifiers

    11. 1022
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de Buyl,E., Lahaye,A., Ledoux,P., Amory,A., Detroz,R., Andre,C. and
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de Buyl,E., Lahaye,A., Ledoux,P., Amory,A., Detroz,R., Andre,C. and
Vetter,R.
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                                                                                                                                           Xylanase derived from a bacillus species, expression vectors for such xylanase and other proteins, host organisms therefor and use thereof
Patent: US 6423523-A 1 23-UU-2002;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                             99.5%; Score 184; DB 6; Length 1022; illarity 100.0%; Pred. No. 1.9e-45; Conservative 0; Mismatches 0; Indels (
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Sequence 35 from patent US 6423523.
AR220053.1 GI:23324471
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563. ...1249
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IGIAFFRQYLSWGTKRTSGTVSVSAHFRKWESLGKFMGKWYETAFTLVNUQPSI
IGIAFFRQYLSV
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Bacillus pumilus endo-1,4-xylanase gene, complete cds.
AF326785
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pumilus HB030
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41.7%; Score 77.2; DB 1; Length 1789;
Best Local Similarity 77.2%; Pred. No. 9.2e-13;
Matches 132; Conservative 0; Mismatches 34; Indels 5
                                                                            Query Match 99.5%; Score 184; DB 6; Length 1022; Best Local Similarity 100.0%; Pred. No. 1.9e-45; Matches 185; Conservative 0; Mismatches 0; Indels
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76 AAAGCAGTATCGTTCCATCTAACAGAAGGNCTGCATGAAAGGAGGTGATGGGTT--TT 133
                             454 AGCACAGTATCGAT--AATCTAATAGTAGGGGCATGAAAGGAGGTGATGAATTCGTT 511
                                                                                 TCATCTTAGGGATGACAGACAATACGGATGAAAAAAGGAGGGATGGAA
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Search completed: November 10, 2004, 21:26:34 Job time : 897.922 secs

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November 10, 2004, 15:55:17 ; Search time 117.352 Seconds (without alignments) 8275.436 Million cell updates/sec
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185
1 TCATGTAACTCGCCTTGATC......AAAAAGGAGAGGGATGGAAA 185
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                   4134886 seqs, 2624710521 residues
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

						SUMMARIES	
			46			•	
Result No.	ult No.	Score	Query	Query Match Length DB	DB	ID	Description
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	-	184	99.5	1022	~	AAQ80923	
	۱ ۸	183	98.9	184	0	AAQ73996	Aaq73996 Xylanase
	n	32.2	17.4	23439	~	AAV74349	Aav74349 Staphyloc
U	4	32	17.3	405	80	ABX38967	Abx38967 Bovine ES
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υ	9	31.6	17.1	28149	'n	ABA17961	Abal7961 Human ner
U	7	31.6	17.1	32192	ß	ABA17963	Abal7963 Human ner
U	60	31.6	17.1	110000	12	ADH69807 4	-
ט	6	31.6	17.1	110000	12	ADH69807_5	Continuation (6 of
	10	31.4	17.0	110000	7	AAV21209 04	Continuation (5 of
	11	31.2	16.9	443	4	AA191410	Aai91410 Human pol
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	13	31	16.8	390	80	ACA11514	Acall514 Human lun
	14	31	16.8	390	80	ACA02700	Aca02700 Lung canc
	15	31	16.8	390	10	ADH46742	Adh46742 Human lun
C	16	31	16.8	410	Ŋ	ABV39054	Abv39054 Human pro
•	17	31	16.8	2262	10	ADF00565	Adf00565 Bacterial
U	18	31	16.8	5124	4	AAK75882	Aak75882 Human imm
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	20	31	16.8	32183	2	ADE46688 .	Ade46688 Human car
U	21	31	16.8	51935	4	AAK75883	Aak75883 Human imm

Abz15647 Arabidops	Adq59207 MSI-H car	Aas68017 DNA encod	Aca28595 Prokaryot	Aca55420 Human sig	Adi55216 Human pol	Aba01445 Streptoco	Aaz92583 Human DAZ	Abl09262 Drosophil		_	Aac44275 Arabidops	_	_	Aas40051 Genomic s		Aah65014 C glutami	U		Abl07432 Drosophil	Aba01094 Brevibact	Abl07438 Drosophil		Continuation (12 o
ABZ15647	ADQ59207	AAS68017	ACA28595	ACA55420	AD155216	ABA01445	AAZ92583	ABL09262	ABL09206	ABQ88146	AAC44275	ACH04273	AAK91468	AAS40051	ADB33011	AAH65014	ACA01823	AAL47164	ABL07432	ABA01094	ABL07438	ABX08336 11	ADJ25985_11
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ALIGNMENTS

RESULT 1

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specification"
                                                                      Xylanase; endo-1,4-beta-D-xylanase; wood pulp; pulping; biobleaching; bleaching; bleaching; bleaching; bacillus licheniformis; ss.
                                                                                                                                                                                                                                                                                                                                                            Amory A, Andre C, De Buyl E, Detroz R, Lahaye A, Ledoux P;
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267. .866
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                                        02-AUG-1995 (first entry)
                                                         B. pumilus xylanase gene.
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                                                                                                   Bacillus pumilus.
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                       AAQ80923;
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                                                                 presequence (AAQ73997) were incorporated into vectors used for the expression of DNA (see AAT16101) coding for a mature, thermostable xylanase (AAR92053) of Bacillus sp. 720/1. The enzyme can be produced in transformed hosts, pref. Bacillus licheniformis or B. pumilus, for use in the paper-pulp, animal feed and baking industries. (Updated on 16-0CT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= d /*tag= d note= "these bases represent a line of missing text in /note= nthese
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given in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGATGGGTTTTTCATCTTAGGGATGACAGAACAATACGGATGAAAAAAGGAGGGAT
                                                                                                                                                                                                                                                                                                                              1 TCATGTAACTCGCCCTTGATCTATTTCATTTGTATCAAAGGATTTATACACAACAAGAGA
                                                                                                                                                                                                                                                                                                                                                                            CATCCATGCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAAAGGNCTGCATGAAAGGA
                                                                                                                                                                                                                                                                                                       61 CATCCATGCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAAGGACGCTGCATGAAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTGATGGGTTTTTCATCTTAGGGATGACAGAACAATACGGATGAAAAAGGAGGGGAT
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                                 Bacillus pumilus PRL B12 xylanase gene promoter (AAQ73996) and
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//note= "chese bases represent a line of missing
/note= "chese bases represent a line of missing
the sequence listing in the specification. They
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the specification for this DNA sequence"
4081. 4140
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/note= "these bases represent a line of missing
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the sequence listing in the specification. They
included to maintain the nucleotide numbering gi
the specification for this DNA sequence"
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0
                                                                                                                                                                                                                                 Length 184;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                             Sequence 184 BP; 63 A; 29 C; 45 G; 46 T; 0 U; 1 Other;
                                                                                                                                                                                                                             98.9%; Score 183; DB 2; I
100.0%; Pred. No. 7.9e-49;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus contig SEQ ID #38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                26; Page 69; 94pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV74349 standard; DNA; 23439
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                                                                                                                                                                                                                                                                    Matches 184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          toxic shock syndrome; ds
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                                                                                                                                                                                                                               Query Match
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              Claim
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                                                                 Purified xylanase from Bacillus pumilus PRL B12 - esp. produced in transformed Bacillus licheniformis, and related DNA, vectors, etc., used for pre-treatment of wood pulp to reduce chlorine or ozone consumption in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTGATGGGTTTTTCATCTTAGGGATGACAGAACAATACGGATGAAAAAAGGAGAGGGAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xylanase; thermostable enzyme; paper; pulp; bleaching; feedstuff; baking;
                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                        A Bacillus pumilus PTL B12 (ATCC 55443) gene library was screened for recombinant plasmids carrying the xylanase gene. A chromosomal fragment obtained from isolate pBPX1 was subcloned and expressed in Escherichia coli JM109. The sequence of the xylanase gene (as a 1022 bp Sau3AI fragment) carried by a selected transformant is given in AAQ80923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus derived xylanase active over wide pH range - used in treatment of paper pulp, animal feeds and in bakery goods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATCCATGCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAAAGGNCTGCATGAAAGGA
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                                                                                                                                                                                                                                                                                                     Sequence 1022 BP; 329 A; 197 C; 229 G; 266 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                                                         6.7e-49;
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                                                                                                                                                                                                                                                                                                                            99.5%; Sco...
100.0%; Pred. No. c...
0; Mismatches
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                                                                                                                                                          Claim 13; Fig 1a-1b; 97pp; English.
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Matches 185; Conservative
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                                                                                                                        subsequent bleaching
              WPI; 1995-039214/06.
P-PSDB; AAR68849.
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17-MAY-1995;
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15-MAY-1996
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AAQ7399(RESULT

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/note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
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/note= "these bases represent a line of missing text in
the sequence listing in the specification. They are
included to maintain the nucleotide numbering given in
the specification for this DNA sequence"
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the sequence listing in the specification. They are included to maintain the nucleotide numbering given the specification for this DNA sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                         the specification for this DNA sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-374922/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JAN-1996;
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Rosen

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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The colypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, evelid infections, food poisoning, osteomyelitis, shin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating computer and production of the polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11481 TATGTATAAACGTGAGTGAGTTAGGCGTTCATTGTTCAGTCGTTGGTGGTGCGATAAC 11540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11541 ACGACCAAAGAAATTACGAAACGTTTTGTTCAAATTATGGAAGATTAAATGATAACGAT 11600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 TATACACAAACAAGAGACATCCATGCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 AGGNCTGCATGAAAGGAGGTGATGGGTTTTTCATCTTAGGGATGACAGAACAATACGGAT
stored on computer readable medium and used in the production of anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23439 BP; 7768 A; 3506 C; 4455 G; 6921 T; 0 U; 789 Other;
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                                                      Claim 1; Page 339-352; 3271pp; English
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11-JAN-2000; 2000US-00480902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 17.4%;
Best Local Similarity 52.2%;
Matches 70; Conservative
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MATHIALAGAN N.
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WARREN W C.
                   S.aureus vaccines.
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                                                                                                                                                                                                                                                                                                                                                                                                               readable medium
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(WARR/)
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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 1512 nuclectide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are (i) in a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non- translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonuclectides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any of the subject of the complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid molecule. The LMFD nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for detection of the molecule. The LMFD nucleic acid is used for detection of the molecule. The LMFD nucleic acid is used for complementary nucleic acid molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle for genetically improving cattle. The present sequence is one of the complementary nucleic acides. The correction but was obtained in pleasing the nucleum of the present sequence as notes the dependent of the nucleum in the specification but was obtained in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 AGTATCGTTCCATCTAACAGAGAAGGNCTGCATGAAAGGAGGTGATGGGTTTTTCATCTT 140
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                                                                                                  New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 405 BP; 138 A; 63 C; 64 G; 139 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              electronic format from the USPTO web site:
segdata.uspto.gov/sequence.html?DocID=20020137139
  Warren WC;
                                                                                                                                                                                                        Claim 2; SEQ ID NO 4132; 245pp; English
  Tao N,
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Mathialagan N,
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                                                    WPI; 2003-110599/10.
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AAA41261 to AAA43419 represent specifically claimed secreted expressed sequence tags (BESTS), isolated from human, mouse, xenopus and rat tissue sources. The BESTS can have a range of activities depending on the tissues they were isolated from. The activities include: chemotaciti; proliferative; immunomodulatory; haematopoietic; chemotanic; analgesic; haemostatic; thrombolytic; antiflammatory; cytostatic; antibacterial; antifungal; antivital; antiflammatory; cytostatic; antibacterial; osteopathic; neuroprotective; nootropic; antibachanismian; antipacriatic; cerebroprotective; nootropic; antibackinsonian; antipacriatic; cerebroprotective; and avacines. The sESTS can be used for gene therapy and in vaccines. The sESTS are useful as probes for molecules which correspond to the sESTS. Proteins encoded by the sESTS are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders antibalish and a set of the second and the second antibacterial and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 AGAGACATCCATGCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAGGAGGACGCATGA 115
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autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myedioid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; parkinson; disease; huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour; infection; depression; psoriasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 AAGGAGGTGATGGGTTTTTCATCTTAGGGATGACAGAACAATACGGATGAAAAAAGGAG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (SESTS), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders.
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Treacy M;
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Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisaickling; antianaemic; antiatriathitic; cancer; antirhemmatic; hepatotropic; cerebroprotective; antiinflammatory; antialergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
                                                Human nervous system related polynucleotide SEQ ID NO 10292
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2000US-0227182P.
2000US-0227009P.
2000US-0228924P.
2000US-0229387P.
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2000US-0225270P.
2000US-022547P.
2000US-0225757P.
2000US-0225758P.
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2000US-0232081P.
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20000S-0189874P

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20000S-0215135P

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20000S-0217487P

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2000US-0217487P

2000US-022518P
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2000US-0180628P.
2000US-0184664P.
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                          (first entry)
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19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
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14-AUG-2000;
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6-SEP-2000;
8-SEP-2000;
8-SEP-2000;
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07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
                                                                                                                                                                          Homo sapiens
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                            23-JAN-2002
  ABA17961;
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antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
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2000US-0190076P.
2000US-0198123P.
2000US-0205515P.
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2000US-0214886P.
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2000US-0225266P.
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                                                          Homo sapiens
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       The invention relates to novel genes (ABA11004-ABA21534) and proteins character and conditions e.g. by protein or gene therapy. The genes are medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.

The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune also ansemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as wycardial isolatemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infections diseases such as viral, bacterial, fungal and parasitic infections Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14557; AGAGGTTTAAATGGGCCTCAAAAAAGTGGCTGCTGCTCCAACAGAGAAAAGCTCTAAAA 14498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 AGAGACATCCATGCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAGGACGCCTGCATGA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianemic; antiarthritic; cancer; antitheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 AAGGAGGTGATGGGTTTTTCATCTTAGGGATGACAGAACAATACGGATGAAAAAAGAG 174
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                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 10292; 1701pp + Sequence Listing; English.
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53.8%; Pred. No. 23;
ative 0; Mismatches
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ID ABA17963 standard; DNA; 32192 BP
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                                                                           ; 2000US-0251479P.
; 2000US-0251856P.
; 2000US-0251868P.
; 2000US-0251869P.
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2000US-0254097P.
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                                       2000US-0251988P.
2000US-0256719P.
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Best Local Similarity 53.8
Matches 64; Conservative
                                                                                                                                                                                                                                                                            Barash SC,
                                                                                                                                                                                                                                                                                                                WPI; 2001-541565/60.
                                                                                                                                                                                                                                                                                                                                                                                       and metastases
   01-DEC-2000; 2
05-DEC-2000; 2
05-DEC-2000; 2
06-DEC-2000; 2
08-DEC-2000; 2
08-DEC-2000; 2
08-DEC-2000; 2
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셤 8 2000US-0234223F 2000US-0234274F

21-SEP-2000; 21-SEP-2000;

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PR 25-SEP-2000; 2000US-0234997P.
PR 27-SEP-2000; 2000US-0235844P.
PR 27-SEP-2000; 2000US-0235834P.
PR 29-SEP-2000; 2000US-0235834P.
PR 29-SEP-2000; 2000US-023534P.
PR 29-SEP-2000; 2000US-023534P.
PR 29-SEP-2000; 2000US-023537P.
PR 29-SEP-2000; 2000US-023704P.
PR 29-SEP-2000; 2000US-023704P.
PR 29-SEP-2000; 2000US-023704P.
PR 29-SEP-2000; 2000US-023704P.
PR 20-CT-2000; 2000US-0241808P.
PR 20-CT-2000; 2000US-0241808P.
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PR 20-CT-2000; 2000US-0241808P.
PR 20-CT-2000; 2000US-0241808P.
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PR 20-CT-2000; 2000US-0241808P.
PR 20-CT-2000; 2000US-0241808P.
PR 20-CT-2000; 2000US-024617P.
PR 20-CT-2000; 2000US-024617P.
PR 20-CT-2000; 2000US-024617P.
PR 20-CT-2000; 2000US-024617P.
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PR 20-CT-2000; 2000US-024617P.
PR 20-CT-2000; 2000US-024617P.
PR 20-CT-2000; 2000US-024617P.
PR 20-CT-2000; 2000US-024617P.
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PR 20-CT-2000; 2000US-024617P.
PR 20-CT-2000; 2000US-024617P.
PR 20-CT-2000; 2000US-024921P.
PR 20-CT-2000; 2000US-024921P.
PR 20-CT-2000; 2000US-024921P.
PR 20-CT-2000; 2000US-024921P.
PR 20-CT-2000; 2000US-024921P.
PR 20-CT-2000; 2000US-024921P.
PR 20-CT-2000; 2000US-024921P.
PR 20-CT-2000; 2000US-024921P.
PR 20-CT-2000; 2000US-024921P.
PR 20-CT-2000; 2000US-024921P.
PR 20-CT-2000; 2000US-024921P.
PR 20-CT-2000; 2000US-024921P.
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PR 20-CT-2000; 2000US-024921P.
PR 20-CT-2000; 2000US-024929P.
PR 20-CT-2000; 2000US-024929P.
PR 20-CT-2000; 2000US-024929P.
PR 20-CT-2000; 2000US-024929P.
PR 20-CT-2000; 2000US-024929P.
PR 20-CT-2000; 2000US-024929P.
PR 20-CT-2000; 2000US-024929P.
PR 20-CT-2000; 2000US-024929P.
PR 20-CT-2000; 2000US-024929P.
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14679-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. CT he mucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and coverian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital, (b) immune of disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, commultiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myccardial ischaemias; (d) wound healing conficus diseases such as wiral, bacterial, fungal and parasitic confections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published_pct_sequences
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                                                                                                                                         Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 GCAGTATCGTTCCATCTAACAGAAGGNCTGCATGAAAGGAGGTGATGGGTTTTTCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 TCTATTTCATTTGTATCAAAGGATTTATACACAAACAAGAGACATCCATGCCGGGTTAAA
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Continuation (5 of 7) of ADH69807 from base 400001 (Human Vbeta gene. )
WP Sequence split into 7 fragments LOCUS ADH69807 Accession Adh69807
WP Fragment Name Begin End
WP ADH69807_0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 32192 BP; 7965 A; 7802 C; 8055 G; 8370 T; 0 U; 0 Other;
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Pred. No. 36;
0; Mismatches
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17.1%; Score 31.6;
Best Local Similarity 53.8%; Pred. No. 24
Matches 64; Conservative 0; Mismatche
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05-JAN-2001; 2001US-0259678P.
                                      (HUMA-) HUMAN GENOME SCI INC.
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200001
300001
400001
500001
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                                                                            Rosen CA, Barash SC,
                                                                                                               WPI; 2001-541565/60.
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ADH69807_1
ADH69807_2
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ADH69807_4
ADH69807_5
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    $X4X1XBXFFFFX8XX8X9X8X5FXBXBXBXBX8X8X8X8
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The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to eytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymerial polymerial in other cell populations. The polymerial polymerial in the respiration or which may induce e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 ACAGAGAAGGNCTGCATGAAAGGAGGTGATGGGTTTTTTCATCTTAGGGATGACAAAAAA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 GGAGGAAAGACAAGAAGAAGGTGAAGAAGAAGAAGGAAGCTAGGGCAGTGCAGAAATG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 aadgaragcaaccaacaacaacaraacaraaarararcrrrrcaaggarrcagcrcraarg 191
                                                                                                               Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 AAGGATTTATACACAAACAAGAGACATCCATGCCGGGTTAAAGCAGTATCGTTCCATCTA
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 443 BP; 143 A; 80 C; 112 G; 108 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.9%; Score 31.2; DE ilarity 50.3%; Pred. No. 7.6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 TACGGATGAAAAAGGAGAGGGATGGAAA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 gagacaaagggaaaagaaaaggaaarcgaga 280
                                                                                   Human polynucleotide SEQ ID NO 11470.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK39185 standard; cDNA; 390 BP.
                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                 28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                                                                  26-FEB-2001; 2001WO-US004927
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-514838/56.
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nes 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AA011479.
                                                                                                                                                                                                                                 WO200164835-A2
                                                                                                                                                                                                    Homo sapiens
                                                   06-NOV-2001
                                                                                                                                                                                                                                                                  07-SEP-2001
                  AAI91410;
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Matches
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ABK39185
ID ABK3
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AC ABK3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92343 GAATCATGTCGATTGAATCGTAGGTTTTATCATCATTTAAGCTACTTACAAGCCTTTCTA 92402
                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                               4161 rccarriccaacricrrrrgraagcrargaacaraaaaacracaragcrrrrgagrgccrgra 4102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                4101 ATAGCAAGATTTTACCTAATTAAAAAGGTTGGGAAAGGAAGTGGCATTTGAGTTGGGTTC 4042
                                                                                                                                                                                                                                                                                                                                                                                                                79 GCAGTATCGTTCCATCTAACAGAGAAGGNCTGCATGAAAGGAGGTGATGGTTTTTCATC 138
                                                                                                                                                                                                                                                                                                                                                  78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16
                                                                                                                                                                                                                                                                                                                                                 19 TCTATTTCATTTGTATCAAAGGATTTATACACAACAAGAGACATCCATGCCGGGTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                               ADH69807 from base 500001 (Human Vbeta gene. fragments LOCUS ADH69807 Accession Adh69807 Begin End
                                                                                                                                                                                                                                                                                Length 110000;
104041 TGAAGGATGAACGGAATGAACTCTGCAAACCCAAGAGAAGAACA 103995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 TTAGGGATGACAGAACAATACGGATGAAAAAGGAGGGGATGGAAA 185
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                  85;
                                                                                                                                                                                                                                                                                 DB 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92403 ATTCAGATTTTTTCTTTCAACTGAGAG 92431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31.4; DI
Pred. No. 42;
0; Mismatches
                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                 Score 31.6; |
Pred. No. 36;
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                                                                                                                                                 1110000
210000
310000
410000
510000
610000
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1610000
1664976
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AA191410
ID AA191410 standard; cDNA; 443 BP.
                                                                                                                    fragments
Begin
                                                                                                                                                                                                                                                                                 17.1%;
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Conservative
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200001
300001
400001
500001
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500001
600001
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1500001
1600001
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                                                                                ADH69807 5/c
Continuation (6 of 7) of
WP Sequence split into 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV21209 04
Continuation (5 of 17) of
WP Sequence split into 1:
WP Fragment Name
WP AAV21209 00
WP AAV21209 02
WP AAV21209 02
WP AAV21209 03
WP AAV21209 04
WP AAV21209 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 53; Conserv
                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                Fragment Name
ADH69807 0
ADH69807 1
ADH69807 2
ADH69807 3
ADH69807 4
ADH69807 6
ADH69807 6
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AAV21209_08
AAV21209_09
AAV21209_10
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AAV21209_14
AAV21209_15
AAV21209_16
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AAV21209_12
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Best Local S
Matches 82
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Matches
                                                                              ADH69807
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Novel lung cancer polynucleotide encoding lung cancer protein, useful for detecting the presence of lung cancer in a patient, and in pharmaceutical compositions, e.g. vaccines, for treating lung cancer.
                                                                                                         Human; lung cancer; ss; lung tumour; cytostatic; vaccine; T cell expansion; CD4; CD8.
                                                                           Human lung adenocarcinoma library cDNA SEQ ID 1223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page; 72pp; English.
                                                                                                                                                                                                                                                        03-MAY-2001; 2001US-00849626.
                                                                                                                                                                                                                                                                                          13-DEC-2000; 2000US-00736457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-352750/33.
                                                                                                                                                                                            US2002197669-A1
                                                                                                                                                               Homo sapiens.
                                               05-JUN-2003
                                                                                                                                                                                                                          26-DEC-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bangur CS,
Clapper JD;
                ACA11514;
                                                                                                                                                                                                                                                                                                                          (BANG/)
(FANG/)
                                                                                                                                                                                                                                                                                                                                                        (WANG/)
(WANG/)
(SWIT/)
(MCNE/)
                                                                                                                                                                                                                                                                                                                                                                                                                          CLAP/)
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes an isolated polynucleotide and polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein for determining the presence of a cancer in a patient. A composition containing the polynucleotide and/or polypeptide is useful for treating a lung cancer in a patient. The polypeptide is useful for removing the polynucleotide sample. The polynucleotide is also useful as probe or primer to detect the level of mRNA encoding a tumour protein. This sequence encodes a lung tumour associated protein or protein. This patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATGAAATCTCTGTTCGTAGCAAGTGCATGTCTCACAGTTGTCAGTCTGCCACTCCGAG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 TTAAAGCAGTATCGTTCCATCTAACAGAGAAGGNCTGCATGAAAGGAGGTGATGGGTTTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Triatregrerrictriccrireagarccarecarriccresingaarcressacre 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mcnabb A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumour; cancer; T cell; immune response stimulator; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polynucleotide encoding a lung tumor polypeptide useful for stimulating and/or expanding T cells specific for a tumor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 CCTCATTAGGTATGAAATAGCATGCATTGCATAAAGTCACGAAGG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 TCATCTTAGGGATGACAGAACAATACGGATGAAAAAAGGAGGAGGATG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                            Johnson JC, Retter MW;
Vedvick TS, Bangur CS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.8%; Score 31; DB 6; Length 390;
48.8%; Pred. No. 8.4;
tive 0; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Watanabe Y, Henderson RA, Johnson JC, Retter is M, Carter D, Fanger GR, Vedvick TS, Bangu: Fanger N, Switzer A, Mcneill PD, Clapper JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 390 BP; 96 A; 92 C; 83 G; 119 T; 0 U; 0 Other;
                                                  cDNA encoding lung tumour protein clone R0131:G04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 1223; 223pp; English.
                                                                                                                                                                                                                                                                                                           26-SEP-2000; 2000US-00671325.
06-OCT-2000; 2000US-00677419.
30-OCT-2000; 2000US-00705.
13-DEC-2000; 2000US-00736457.
03-MAY-2001; 2001US-00849626.
                                                                                                                                                                                                                             10-JUL-2001; 2001WO-US022058
                                                                                                                                                                                                                                                                                2000US-00651563
2000US-00658824
                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 48.8
                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-164634/21
                                                                                                                                                                 WO200204514-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang T, Watana
Marnerakis M,
                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                               11-JUL-2000;
                                                                                                                                                                                                                                                                                29-AUG-2000;
08-SEP-2000;
                     21-MAY-2002
                                                                                                                                                                                                 17-JAN-2002
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                                                                                                      gene;
                                                                                    Lung
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Switzer AP, Mcneill PD;

Wang A, Wang T,

Fanger GR,

SWITZER A I MCNEILL P I CLAPPER J I WANG A.

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BANGUR FANGER

Comprision relates to a polymuciacolide and ung fundur protein, comprising a sequence selected from any of the 14 sequences mentioned in the invention relates to a sequence (S2) mentioned in specification, or a sequence (S2) mentioned in specification, or a sequence consisting of at least 20 contiguous residues of S1, sequences that hybridise to S1, sequences having 75%, preferably CC S1, sequences mentioned in the specification, a sequence (S3) selected from any one of the 4 amino acid sequences mentioned in the specification, a sequence comprising a sequence (S3) selected from any one of the 4 amino acid sequences mentioned in the specification, a sequence comprising the polymucleotide operably linked to an expression vector comprising the polymucleotide operably linked to an expression ocntrol sequence, a host cell transformed or transfected with the vector, an isolated antibody (or its antigen-binding fragment) that expression control sequence, a host cell transformed or transfected with the vector, an isolated antibody (or its antigen-binding fragment) that conditions stimulating and/or expanding T cells with the polymucleotide, protein or antigen-presenting cells that hybridises to S1 under moderately stringent conditions stimulating and/or expanding T cells specific for a tunour processoring colls that madvor expansion of T cells) and inhibiting the presenting cells that express the polymucleotide, protein or antigen or expension and/or expansion of T cells) and inhibiting the expression for stimulateing to the patient an effective amount of the proliferated T cells, and thus inhibiting the development of a cancer in a patient (particularly lung cancer). The protein and oligonucleotide, protein and allo useful in pharmaceutical composition for stimulateing an immune response in a patient. The protein and oligonucleotide is also useful in pharmaceutical compositions, e.g. vaccines the polymucleotide is also useful in pharmaceutical cor primer for nucleic acid hybridisation, and in the design and cor prime The invention relates to a polynucleotide encoding a lung tumour protein.

ACA11514 standard; cDNA; 390 BP.

RESULT 13 ACA11514 ID ACA1

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25-MAR-2004
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  a suitable
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                                                                                                                                                                                                                               235 TITTATTGGTGTTTGTTTCCTTTGAGATCCATGCATTTCCTGGTTGAATCTCCTGGAACTC 294
polynucleotide is useful for isolating a full-length gene from a suitable library. The present sequence is a cDNA (full length, extended or partial) isolated from a library derived from lung tumour/cancer cells. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                         73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or
                                                                                                                                                        TTAAAGCAGTATCGTTCCATCTAACAGAGGACGNCTGCATGAAAGGAGGTGATGGGTTTTT
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotide, useful for preparing a composition for treating inhibiting development of cancer, e.g. lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mcnabb
                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer; cytostatic; vaccine; gene therapy; cancer; gene; ss
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                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                             295 ccrcarradgraridaaaragcargargcarracaraaagrcacgaagg 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y, Johnson JC, Retter MW;
Vedvick TS, Bangur CS, M
                                                             USPTO at segdata.uspto.gov/sequence.html?DocId=20020197669
                                                                                                        Score 31; DB 8; Length 390; Pred. No. 8.4;
                                                                                                                                                                                                                                                       TCATCTTAGGGATGACAGAACAATACGGATGAAAAAAAGGAGAGGGTG
                                                                                                                                 86; Indels
                                                                                    Sequence 390 BP; 96 A; 92 C; 83 G; 119 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                             Lung cancer therapyand diagnosis associated cDNA #1189
                                                                                                          16.8%; Score 31; DB
llarity 48.8%; Pred. No. 8.4;
Conservative 0; Mismatches
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Fanger GR,
                                                                                                                                                                                                                                                                                                                                           ВР
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2000US-00533077.
2000US-00546259.
2000US-00560406.
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99US-00419356.
99US-00466867.
99US-00476300.
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2000US-00651563.
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2000US-00671325.
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                                                                                                                                                                                                                                                                                                                                         ACA02700 standard; cDNA; 390
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03-MAY-2001; 2001US-00849626
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Carter D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-328427/31
                                                                                                                      Best Local Similarity
Matches 82; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2002172952-A1
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22-MAR-2000;
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27-APR-2000;
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29-AUG-2000;
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17-DEC-1999;
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The invention relates to novel compositions and methods for the therapy and diagnosis of cancer, particularly lung cancer. The compositions comprise one or more lung tumour polypeptides, immunogenic portions therof, polynculeotides that encode such polypeptides, antigen presenting cells that express such polypeptides, and T cells that are specific for cells expressing such polypeptides. The novel compositions have cytostatic and immunostimulant activity. The lung tumour antigens can be
                                                                                                                                                                                                                                         ö
                              The invention describes an isolated polynucleotide comprising one of 32 sequences, complement or degenerate variants of them. The polynucleotide is useful for preparing a composition e.g. a vaccine or for gene therapy, for treating or inhibiting development of cancer, e.g. lung cancer. This sequence represents a polynucleotide associated with the compositions and methods for the therapy and diagnosis of lung cancer
                                                                                                                                                                                                                                                                                                               234
                                                                                                                                                                                                                                                                                                                                                    TTAAAGCAGTATCGTTCCATCTAACAGAAGGNCTGCATGAAAGGAGGTGATGGGTTTT 133
                                                                                                                                                                                                                                                                                                                                                                                       235 TTTATTGGTGTTTGTTTCCTTTGAGATCCATGCATTTCCTGGTTGAATCTCCTGGAACTC 294
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                                                                                                                                                                                                                                                                                                                 175 CATGAAATCTCTGTTTCGTAGCAAGTGCATGTCTCACAGTTGTCAGTCTGCCACTCCGAG
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Fanger GR,
                                                                                                                                                                                                     Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                             134 TCATCTTAGGGATGACAGAACAATACGGATGAAAAAGGAGAGGGATG
                                                                                                                                                                                                                                         86; Indels
                                                                                                                                                              Sequence 390 BP; 96 A; 92 C; 83 G; 119 T; 0 U; 0 Other;
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Pred. No. 8.4;
0; Mismatches 8
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Carter I
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Example 1; SEQ ID NO 1223; 82pp; English.
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Best Local Similarity 48.8%;
Matches 82; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; cDNA; 390
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Retter MW,
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Monabb A;
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                                                                                                                                                                                                                                                                                                     used in the creation of a vaccine. The polynucleotides that encode the lung tumour polypeptides can be used in gene therapy to help in the treatment of lung tumours. This polynucleotide sequence represents a human lung tumour DNA clone of the invention. This sequence was not shown in the specification. It has been taken from a World Intellectual Property Organization CD ROM supplied with the specification.
                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                         Query Match 16.8%; Score 31; DB 10; Length 390; Best Local Similarity 48.8%; Pred. No. 8.4; Matches 82; Conservative 0; Mismatches 86; Indels
                                                                                                                                                             Sequence 390 BP; 96 A; 92 C; 83 G; 119 T; 0 U; 0 Other;
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Search completed: November 10, 2004, 17:09:37 Job time : 121.352 secs

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Sequence 28, Application US/08275526C

Patent No. 6180382

GENERAL INFORMATION:
APPLICANT: LAHAYE, ANDR E
APPLICANT: LAHAYE, ANDR E
APPLICANT: AMORY, ANTONE
APPLICANT: AMORY, ANTONE
APPLICANT: AMORY, ANTONE
APPLICANT: AMORY, ANTONE
APPLICANT: AMORY, ANTONE
APPLICANT: AMORY, ANTONE
APPLICANT: AMORY, ANTONE
APPLICANT: AMORY REN
TITLE OF INVENTION: EXPRESSION VECTORS FOR SUCH XYLANASE AND
TITLE OF INVENTION: OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
TITLE OF INVENTION: USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STRATE: D.C.
COUNTRY: U.S.A.
ITP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OMPUTER: PLOPPY disk
COMPUTER: IBM PC compatible
OMPUTER: PLOPPY disk
COMPUTER: IBM PC compatible
OMPUTER: IBM PC compatible
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COMPUTER: IBM PC compatible
OMPUTER: IBM PC compatible
OMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OMPUTER: IBM PC compatible
OMPUTER: STEMIN NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 37,136
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US-08-275-526C-28
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Sequence 18, Appa
Sequence 38, Appl
Sequence 1, Appli
Sequence 1, Appli
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Sequence 1223, Ap
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Sequence 35, Appl
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Sequence 18, Appl
Sequence 101, App
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Sequence 1, Appli
Sequence 35, Appl
                                                                                                                                November 10, 2004, 17:09:58 ; Search time 21.2524 Seconds (without alignments) 6187.359 Million cell updates/sec
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185
1 TCATGTAACTCGCCTTGATC......AAAAAGGAGAGGGATGGAAA 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Issued Patents NA:*

... /cgn2 6/ptodatca/1/ina/5A_COMB.seq:*
... /cgn2 6/ptodatca/1/ina/6A_COMB.seq:*
... /cgn2 6/ptodatca/1/ina/6A_COMB.seq:*
... /cgn2 6/ptodatca/1/ina/6B_COMB.seq:*
... /cgn2 6/ptodatca/1/ina/PcTUS COMB.seq:*
... /cgn2 6/ptodatca/1/ina/PcTUS COMB.seq:*
... /cgn2 6/ptodatca/1/ina/PcTUS COMB.seq:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-736-457-1223
US-09-671-1248-1223
US-09-671-325-1223
US-09-671-325-1223
US-09-543-681A-850
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US-08-742-185-101
US-09-248-796A-6234
US-09-950-071-1
US-08-845-258-3
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US-09-073-055-28
US-08-275-526C-1
US-08-076-677-1
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US-09-692-570-1
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Maximum Match 100%
Listing first 45 summaries
                                                                                            nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Match Length DB
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28.4
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Maximum DB
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genomic DNA

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40, Appl
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11, Appli
4, Appli
4, Appli
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                                                                                                           1383, Ap
                                                  Sequence 3
Sequence 4
Sequence 6
                                                                        Sequence Sequence 1
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Sequence
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   US-08-990-571-3

US-08-990-571-40

US-08-723-142A-43

US-08-723-142A-40

US-09-528-784A-40

US-09-558-784A-40

US-09-569-098A-3

US-09-143-127-6

US-09-143-127-6

US-09-143-127-1

US-08-976-16A-4

US-08-976-16A-4

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US-08-976-16A-4
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 2430
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2430
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24430
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120

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61 CATCCATGCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAGAAGGACTGAAAGGA 120
                                                                                                                                                                                        121 GGTGATGGGTTTTTCATCTTAGGGATGACAGAACAATACGGATGAAAAAAGGAGAGGGGAT 180
                                                                                                         CATCCATGCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAAGGNCTGCATGAAAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXPRESSION VECTORS FOR SUCH XYLANASE AND OTHER PROTEINS, HOST ORGANISMS THEREFOR AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.5%; Score 184; DB 4; Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE,
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20006
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 12-May-1998
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/275,526
FILING DATE: 15-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gadiano, Wilhlem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: genomic DNA SEQUENCE DESCRIPTION: SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202) 429-0625
TELEFARA: (202) 293-0625
TELERA: 650 383 5605
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMORY, ANTOINE
DETROZ, RENE
ANDRE, CHRISTOPHE
VETTER, ROMAN
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28, Application US/09076677
Patent No. 6423523
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 185 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
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LAHAYE, ANDREE
LEDOUX, PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 35
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TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase
TITLE OF INVENTION: and uses thereof
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
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                                           0; Gaps
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  Length 185;
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                                         Indels
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ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,953A
TILING DATE: 6-OCTOBER-1995
Query Match 99.5%; Score 184; DB 3; L.
Best Local Similarity 100.0%; Pred. No. 5.7e-52;
Matches 185; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 5.7e-52;
Matches 185; Conservative 0; Mismatches 0;
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US-08-470-953A-26
Sequence 26, Application US/08470953A
; Parent No. 6346407
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ATTORNEY/AGENT INFORMATION:
NAME: WIlhlem F. Gaddano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-
TELECHONICATION INFORMATION:
TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARGERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: DNA (genomic)
US-08-470-953A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: ANDREE LAHAYE
APPLICANT: BRIC DE BUYL
APPLICANT: PIERRE LEBOUX
APPLICANT: RENE DETROZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 185 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STATE: D
COUNTRY:
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99.5%; Score 184; DB 4; 1
100.0%; Pred. No. 5.7e-52;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Gadiano, Wilhlem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 412
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37,136
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STRAIN: PRL B12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: genomic DNA ORIGINAL SOURCE:
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LAHAYE, ANDR E
LEDOUX, PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202) 299-0625
TELEX: 650 383 5605
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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                              Best Local Similarity 100.
Matches 185; Conservative
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TITLE OF INVENTION: EXP
TITLE OF INVENTION: USE
TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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US-08-275-526C-1
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                                                     Gaps
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EXPRESSION VECTORS FOR SUCH XYLANASE AND
CTHER PROTEINS, HOST ORGANISMS THEREFOR AND
USE THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C. STREET: 2000 K St., N.W., Suite 200 CITY: Washington STATE: D.C.
                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION WHOBER: US/09/073,055
FILING DATE: 05-May-1998
CLASSIFICATION: <UNknown>
100.0%; Pred. No. 5.7e-52; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/275,526
PILING DATE: 15-JUL-1994
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NAME: Gadiano, Wilhlem F.
REGISTRATION NUMBER: 37,136
REPERENCE/DOCKET NUMBER: 4121-49
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: (202) 429-0625
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MOLECULE TYPE: genomic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-073-055-28
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28, Application US/09073055
Patent No. 6426211
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELEX: 650 383 5605
INFORMATION FOR SEQ ID NO: 28:
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DETROZ, REN
ANDRE, CHRISTOPHE
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LENGTH: 185 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DE BUYL, ERIC
LAHAYE, ANDR E
LEDOUX, PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROMAN
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                    Matches 185; Conservative
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   Best Local Similarity
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61 CATCCATGCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAAAGGNCTGCATGAAAGGA 120
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                                                                                                                                                    Gaps
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Length 185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OMPUTER: TEM FOC Compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/275,526C
FILING DATE: 15-JUL-1994
CLASSIFICATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Query Match
Best Local Similarity 100.
Matches 185; Conservative
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                                                                                                                                                                                                                                  GGTGATGGGTTTTTCATCTTAGGGATGACAGAACAATACGGATGAAAAAAGGAGGGGAT 180
                                                                                                                                                                                                                                                         61 CATCCATGCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAAAGGNCTGCATGAAAGGA 120
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXPRESSION VECTORS FOR SUCH XYLANASE AND OTHER PROTEINS, HOST ORGANISMS THEREFOR AND USE THEREOF 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XYLANASE DERIVED FROM A BACILLUS SPECIES
                                  Length 1022;
                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/275,526C
FILING DATE: 15-ULL-1994
                                                 Pred. No. 1.2e-51;
                                  99.5%; Score 184; DB 3;
                                          100.0%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 35, Application US/08275526C Patent No. 6180382 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Gadiano, Wilhlem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMORY, ANTOINE
DETROZ, REN
ANDRE, CHRISTOPHE
VETTER, ROMAN
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TELEFAX: (202) 293-0625
TELEX: 650 383 5605
INFORMATION FOR SEQ ID NO: 35
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DE BUJL, ERIC
APPLICANT: LAHAYE, ANDR E
APPLICANT: LEDOUX, PIERRE
APPLICANT: AMORY, ANTOINE
APPLICANT: ANDRE, CHRISTOPH
APPLICANT: ANDRE, CHRISTOPH
APPLICANT: VETTER, CRRISTOPH
TITLE OF INVENTION: XYLANA
TITLE OF INVENTION: EXPREST
TITLE OF INVENTION: USE THI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: genomic DNA US-08-275-526C-35
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LEDOUX, PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1022 base pairs
                                Query Match
Best Local Similarity 100.
Matches 185; Conservative
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EDNESS: single
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CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                 GGAAA 185
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 US-08-275-526C-1
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61 CATCCATGCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAGAAGGNCTGCATGAAAGGA 120
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                                                                                         Gaps
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EXPRESSION VECTORS FOR SUCH XXLANASE AND
OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
NUMBER OF SEQUENCES: 35
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ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
Length 1022,
                                                Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/09/076,677
FILING DATE: 12-May-1998
CLASSIFICATION: <URANOWn>
PRIOR APPLICATION: <URANOWN>
  99.5%; Score 184; DB 3; 100.0%; Pred. No. 1.2e-51; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/275,526
FILING DATE: 15-UL-1994
ATTORNEY, AGENT INFORMATION:
NAME: Gadiano, Wilhlem F.
REGISTRATION NUMBER: 37,136
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMORY, ANTOINE
DETROZ, RENE
ANDRE, CHRISTOPHE
VETTER, ROMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202) 293-0625
TELEX: 650 383 5605
INFORMATION FOR SEQ ID NO: 1:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1022 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DE BUYL, BRIC
LAHAYE, ANDREE
LEDOUX, PIERRE
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61 CATCCATGCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAGAAGAAGCACTGCATGAAAGGA 120
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                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INVENTION: XYLANASE DERIVED FROM A BACILLUS SPECIES,
EXPRESSION VECTORS FOR SUCH XYLANASE AND
OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
                                                                                                                                                                     ;
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                                                                                                                            99.5%; Score 184; DB 4; Length 1022; 100.0%; Pred. No. 1.2e-51; tive 0; Mismatches 0; Indels o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.

CONPUTER READABLE FORM:
MIDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NAMBER: US/09/073,055
FILING DATE: 05-May-1998
CIASSIFICATION NATA:
PRIOR APPLICATION NAMBER: US/08/275,526
FILING DATE: 15-UNL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Gadiano, Wilhlem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-49
TELECOMMUNICATION INFORMATION:
TELEFRONE: (202) 299-0625
TELEFAX: (502) 293-6625
      STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMORY, ANTOINE
DETROZ, REN
ANDRE, CHRISTOPHE
VETTER, ROMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09073055
Patent No. 6426211
GENERAL INFORMATION:
APPLICANT: DE BUYL, ERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAHAYE, ANDR E
LEDOUX, PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 185; Conservative
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                                                                                            US-09-076-677-35
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EXPRESSION VECTORS FOR SUCH XYLANASE AND
OTHER PROTEINS, HOST ORGANISMS THEREFOR AND
USE THEREOF
                                                                                                                                         .
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ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                              Length 1022;
                                                                                                                                       Indels
                                                                                                                                           .
0
                                                                                            Query Match
99.5%; Score 184; DB 4; I
Best Local Similarity 100.0%; Pred. No. 1.2e-51;
Matches 185; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,677
FILING DATE: 12-MAy-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/275,526
FILING DATE: 15-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-49
TELEPHONE: (202) 429-0625
TELEPHONE: (202) 293-0625
TELERAX: (202) 293-0625
TELERX: 650-383-5605
INFORMATION FOR SEQ ID NO: 35:
                   STRAIN: PRL B12
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
ORGANISM: Bacillus pumilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DE BUYL, ERIC
LAHAYE, ANDREE
LEDOUX, PIERRE
AMORY, ANTOINE
DETROZ, RENE
ANDRE, CHRISTOPHE
VETTER, ROMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Gadiano, Wilhlem F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 35, Application US/09076677
Patent No. 6423523
GENERAL INFORMATION:
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US-09-076-677-1
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TELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                               Gaps
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CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K St., N.W., Suite 200
                                                                                                                                                                                                                          Length 1022;
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                        Query Match 99.5%; Score 184; DB 4; I
Best Local Similarity 100.0%; Pred. No. 1.2e-51;
Matches 185; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/275,526
FILING DATE: 15-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gadiano, Wilhlem F.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/073,055
FILING DATE: 05-May-1998
CLASSIFICATION: <UNKNOWN>
                                                                                                                           ORGANISM: Bacillus pumilus
STRAIN: PRL B12
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-09-073-055-35
; Sequence 35, Application US/09073055
; Patent No. 6426211
; GENERAL INPORMATION:
; APPLICANT: DE BUYL, ERIC
; APPLICANT: DE BUYL, PIERE
; ANTOINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANDRE, CHRISTOPHE VETTER, ROMAN INVENTION: XYLANASE
                     LENGTH: 1022 base pairs
                                                                       TOPOLOGY: linear MOLECULE TYPE: genomic DNA ORIGINAL SOURCE:
                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMORY, ANTOINE
DETROZ, REN
SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CATCCATGCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAGAAGGNCTGCATGAAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                           Length 1022;
                                                                                                                                                                                                                                                                                                                                                                              Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
                                                                                                                                                                                                                                                                                                                           Query Match
99.5%; Score 184; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.2e-51;
Matches 185; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CORRESPONDENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
APPLICATION NUMBER: BP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT. Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 30472/114 IMMU
TELECHOMINICATION INFORMATION:
TELECHOMINICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: FOLCY & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STAID.
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TYPE: Floppy disk
TYPE: Floppy disk
TYPE: Floppy disk
TYPE: Floppy disk
TYPE: Floppy disk
TYPE: Floppy disk
TYPE: Floppy disk
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Patent No. 5670367
GENERAL INFORMATION:
TELEFAX: (202) 239-0625
TELEX: 650 383 5605
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 1022 base pairs
                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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11481 TATGTATAAACGTGTGATGGACTTAGGCGTTCATTGTTCAGTCGTTGGTGGTGGTGATAAC 11540
                                                                                                                                                                                                                                                                                                       11541 Accaccaaaacaaatraccaaaccrrrrcrararrarccaacarraaargaraaraaarcaar 11600
                                                                                                                                                                                                                       11481 TATGTATAAACGTGATGGACTTAGGCGTTCATTGTTCAGTCGTTGGTGGTGGTAAC 11540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 TATACACAAACAAGAGACATCCATGCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAGA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 AGGNCTGCATGAAAGGAGGTGATGGGTTTTTCATCTTAGGGATGACAGAACAATACGGAT 163
                                                                                                                                                                                                                                                                104 AGGNCTGCATGAAAGGAGGTGATGGGTTTTTCATCTTAGGGATGACAGAACAATACGGAT 163
                                                                                                                                                                                  44 TATACACAAACAAGACATCCATGCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAGA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 38, Application US/08781986A
Parent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
                                                                                                                                           Gaps
                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 23439;
                                                                                                   DB 4; Length 23439;
                                                                                                                                        64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32.2; DB 4;
Pred. No. 1.5;
                                                                                                 Query Match
17.4%; Score 32.2; Di
Best Local Similarity 52.2%; Pred. No. 1.5;
Matches 70; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSEE: Human Genome Sciences, Inc. ; 9410 Key West Avenue Rockville
TOPOLOGY: linear sEQ ID NO: 38: US-08-956-171E-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette, 3.50 inch, 1. COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFRENCE/DOCKET NUMBER: PB244
TELECOMMUNICATION INPORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
                                                                                                                                                                                                                                                                                                                                                       164 GAAAAAAGGAGAGG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 52.2
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
TAPPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Gen
STREET: 9410 Key Wes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20850
COMPUTER READABLE FORM:
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY:
US-08-781-986A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-781-986A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
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Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                              82 GTATCGTTCCATCTAACAGAGGAGGNCTGCATGAAAGGAGGTGATGGGTTTTTCATCTTA 141
                                                                                                                                                                                                                                                                                                                  22 ATTICATITGIATCAAAGGATTIATACACAAACAAGAGACATCCATGCCGGGTTAAAGCA
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                    DB 1; Length 7218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 GGGATGACAGAACAATACGGATGAAAAAGGAGGAGGGATGGAAA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS, version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                             61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                               Query Match
19.4%; Score 35.8; DB 1
Best Local Similarity 15.2%; Pred. No. 0.059;
Matches 25; Conservative 78; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Mark J. Hyman

REGIGSHATTON WINBER: 46,789

REFERENCE/DOCKET NINBER: PB248P1

TELECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 38, Application US/08956171E Patent No. 6593114 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 23439 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patrick S. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Charles Kunsch
Gil H. Choi
                                                                 7218 base pairs
    TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                               LENGTH: 7218 base pair
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                     ; CLONE: pTZgpt-F1s
US-08-232-463-14
                                                                                                                                                 IMMEDIATE SOURCE
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LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (309398). (309398)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (309418). (309418)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (312837). (312837)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (312993). (312993)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (319226). (319226)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (319226). (319226)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc_feature
LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a, t
            INFORMATION: n equals a,
                                                                                            NAME/KEY: misc feature
LOCATION: (234187)..(234187)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (559167)..(559167)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCATION: (674435)..(674435)
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LOCATION: (682442) ..(682442)
OTHER INFORMATION: n equals a,
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LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a,
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LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a,
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LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a,
                              CEY: misc feature
ION: (231980)..(231980)
INFORMATION: n equals a,
                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (234220)..(234220)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                       ION: (234814) .. (234814) INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a,
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INFORMATION: n equals a,
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                                                                                                                                                                                                                                                                                   GENERAL INCORNATION:
APPLICANT: Bult et al.
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ arcter No. 6503729
TITLE OF INVENTION: jannaschii
FILE OF INVENTION: jannaschii
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT APPLICATION NUMBER: US 60/024,428
PRIOR PILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Pacentin version 3.1
SEQ ID NO: 3
NAME/KEY: misc feature
LOCATION: (28222) .. (28222)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (28257) .. (28258)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (84773) .. (84773)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (84808) .. (84808)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (98266).
(198266)
NAME/KEY: misc feature
LOCATION: (98343).
CCATION: (98343).
CCATION: (98343).
CCATION: (198343).
CCATION: (198343).
NAME/KEY: misc feature
LOCATION: (103989). (103998)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc feature
LOCATION: (148948). (148948)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc feature
LOCATION: (148348). (148948)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc feature
LOCATION: (163385). (163385)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc feature
LOCATION: (191999). (191989)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc feature
LOCATION: (191999). (191995)
                                                                                                                                                                                                                                           Sequence 1, Application US/08916421B Patent No. 6503729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (84812). (84912)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (98120). (99120)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (98159). (98159)
OTHER INFORMATION: n equals a, t,
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LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals a,
                                                                                                                     11601 AAAAAACGAGATG 11614
                                                                        164 GAAAAAGGAGAGG 177
                                                                                                                                                                                            RESULT 14
US-08-916-421B-1
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OTHER INFORMATION: n equals a, t, c,
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                                         ORGANISM: Methanococcus jannaschii
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LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a, t,
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LOCATION: (163385)..(163385)
OTHER INFORMATION: n equals a,
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LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals a,
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LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a,
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LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a,
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LOCATION: (191995)...(191995)
OTHER INFORMATION: n equals a,
                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a,
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LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a,
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LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a,
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ION: (84812)..(84812)
INFORMATION: n equals a,
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LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals
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LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals
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LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals
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ION: (98239)..(98239)
INFORMATION: n equals
                                                                             MAME/KEY: misc feature
LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LENGTH: 1664976
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LOCATION:
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Batent No. 6797466
GRNERAL INFORMATION:
APPLICATION:
TITLE OF INVENTION:
COMPLET BULL et al.
TITLE OF INVENTION:
APPLICATION OF 1977466
TITLE OF INVENTION: Januaschii
FILE REPERBUCE: PROJECT
CURRENT PILING DATE: 2003-01-14
PRIOR PILING DATE: 1996-08-22
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTION OF 2003-01-14
ROME PILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN OF 2003-01-14
ROME OF 2003-01-14
ROME PILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 17.0%; Score 31.4; DB 4; Length 1664976; Best Local Similarity 59.6%; Pred. No. 17; Matches 53; Conservative 0; Mismatches 36; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     492403 ATTCAGATTTTTCTTTTCAACTGAGAAG 492431
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LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (1664854)..(1664855)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (1603734). (1603734)
OTHER INFORMATION: n equals a, t, c, or
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                    LOCATION: (1095846)...(1096846)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
                                                                                  COCATION: (1119881). (1119881)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (1130881). (1130881)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (1310988). (1310988)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (1313224). (1313224)
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LOCATION: (1569020). (1569020)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
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LOCATION: (1349491)..(1349491)
OTHER INFORMATION: n equals a,
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LOCATION: (1470091)..(1470091)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a, t,
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LOCATION: (713552)..(713652)
OTHER INFORMATION: n equals a, t,
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LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a, t,
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LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a, t,
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LOCATION: (312837)..(312837)
OTHER INFORMATION: n equals a,
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LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a,
LOCATION: (234220)..(234220)
OTHER INFORMATION: n equals a,
                                                    NAME/KEY: misc_feature
LOCATTON: (234814)..(234814)
OTHER INFORMATION: n equals a,
FEATURE:
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LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a,
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LOCATION: (309418)...(309418)
OTHER INFORMATION: n equals a,
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LOCATION: (312993)..(312993)
OTHER INFORMATION: n equals a,
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LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a,
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LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (657203)
OTHER_INFORMATION: n equals a,
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LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a,
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LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a,
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LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a,
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LOCATION: (559167)..(559167)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc feature
LOCATION: (779576)..(779676)
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492343 GAATCATGTCGATTGAATCGTAGGTTTTATCATCATTTAAGCTACTTACAAGCCTTTCTA 492402
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17.0%; Score 31.4; DE
Best Local Similarity 59.6%; Pred. No. 17;
Matches 53; Conservative 0; Mismatches
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NAME/KEY: misc_feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g
      or g
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LOCATION: (1313224)..(1313224)
OTHER INFORWATION: n equals a, t, c, or
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NAME/KEY: misc_feature
LOCATION: (1310988)...(1310988)
OTHER INFORMATION: n equals a, t,
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LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t,
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LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t,
OTHER INFORMATION: n equals a, t,
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NOAME/KEX: misc_feature
NOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a,
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LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a,
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LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a,
                                     NAME/KEY: misc feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals
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Search completed: November 11, 2004, 01:34:27 Job time : 25.2524 secs

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RESULT 1
US-09-909-207-26
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185
1 TCATGTAACTCGCCTTGATC......AAAAAGGAGAGGGATGGAAA 185
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1: /cgn2_6/ptodata/1/pubpna/VS07 PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/VS06_NEW PUB.seq:*
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18: /cgn2_6/ptodata/1/pubpna/VS0_NEW_PUB.seq:*
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19: /cgn2_6/ptodata/1/pubpna/VS0_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/VS0_NEW_PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Se)9848 Sequence 209848,				Sequence 84, Appl		51	1036 Sequence 41036, A	3 Sequence 38, Appl	Sequence 38, Appl
ΩΙ	9 US-09-909-207-26	US-10-027-632-209848	US-10-027-632-20	US-10-027-632-18	US-10-027-632-18	US-10-369-493-46834	US-10-388-838-84	US-10-424-599-8116	US-10-424-599-141151	US-10-369-493-41036	US-08-781-986A-38	16 US-10-329-624-38
DB	6	13	15	13	15	15	17	16	16	15	œ	
Query Match Length DB ID	185	634	634	624	624	1500	260803	445	355	17.7 3045	23439	23439
Query Match	99.5	20.0	20.0	18.9	18.9	18.8	17.9	17.8	17.7	17.7	17.4	17.4
Score	184	37	37	35	35	34.8	33.2	33	32.8	32.8	32.2	32.2
Result No.		0	ო ს	Ω	C)	9	0 7	ω	0	10	11	12

Sequence 4132, Ap			Sequence 1, Appli	Sequence 72247, A	Sequence 115848,	Seguence 1223, Ap	'n	1223,		1223	ຕັ	494, A	1494,	Sequence 1494, Ap	ij	Sequence 195, App	Sequence 128655,	Sequence 128655,	ന					2825		Sequence 264187,	Sequence 264187,		6389		e 948,	Sequence 49, Appl
US-09-960-352-4132	US-10-027-632-117073	US-10-027-632-117073	US-09-263-959-1	US-10-425-115-72247	US-10-424-599-115848	US-09-736-457-1223	US-09-902-941-1223	US-09-849-626-1223	US-10-017-754-1223	US-10-113-872-1223	US-10-283-017-1223	US-09-764-869-1494	US-10-091-504-1494	US-10-227-577-1494	US-10-428-487-11	US-10-367-094-195	US-10-027-632-128655	US-10-027-632-128655	US-09-938-842A-3452	US-09-938-842A-3452	US-10-087-192-496	US-10-282-122A-16465	US-10-027-632-282580	US-10-027-632-282580	US-10-305-720-18	US-10-027-632-264187	US-10-027-632-264187	US-10-450-826-53		US-10-116-802-478	US-09-764-872-948	US-09-738-626-49
6	13	15	6	18	16	σ	6	0	14	15	15	6	14	16	16	17	13	15	σ	11	13	16	13	15	16	13	15	17	18	14	10	σ
405	1079	1079	684973	326	497	390	390	390	390	390	390	32183	32183	32183	301692	310268	804	804	1132	1132	58723	930	561	561	831	646	646	178896	422	610	977	1143
17.3	17.1	17.1	17.1	16.9	16.9	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.6	16.6	16.6	16.6	16.5	16.3	16.2	16.2	16.2	16.1	16.1	16.1	16.0	16.0	16.0	16.0
32	31.6	31.6	31.6	31.2	31.2	31	31	31	31	31	31	31	31	31	31	31	30.8	30.8	30.8	30.8	30.6	30.2	30	30	30	29.8	29.8	29.8	29.6	29.6	29.6	29.6
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ALIGNMENTS

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TITLE OF INVENTION: Xylanase, microorganisms produced it,
DNA molecule, processes for preparation of this xylanase
and uses thereof
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ZIP: 2006
COMPUTER: 10-20
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 10-20
COMPUTER: 10-20
COMPUTER: 10-20
COMPUTER: 10-20
COMPUTER: 10-20
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/909,207
FILING DATE: 19-3ul-2001
CLASSIFICATION: cUnknown>
                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE STREET: 2000 K St., N.W., Suite 200
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/470,953
FILING DATE: 06-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
Sequence 26, Application US/09909207; Patent No. US20020115181A1
GENERAL INFORMATION:
                                                                          APPLICANT: ANDREE LAHAYE
ERIC DE BUYL
PIERRE LEDOUX
RENE DETROZ
                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 29
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36 AAAGGATTTATACACAAACAAGAGACATCCATGCCGGGTTAAAGCAGTATCGTTCCATCT
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Best Local Similarity
Matches 79; Conserva
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US-10-027-632-182736/c
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Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION:
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPRENCE: 108827.129
CURRENT APPLICATION NUMBER: US 60/218,006
FRICR APPLICATION NUMBER: US 60/198,676
FRICR FILING DATE: 2000-07-12
FRICR FILING DATE: 2000-07-12
FRICR FILING DATE: 2000-03-29
FRICR FILING DATE: 2000-03-29
FRICR FILING DATE: 2000-03-29
FRICR FILING DATE: 1999-11-23
FRICR FILING DATE: 1999-11-23
FRICR FILING DATE: 1999-11-23
FRICR FILING DATE: 1999-108-09
FRICR FILING DATE: 1999-108-09
FRICR FILING DATE: 1999-108-09
FRICR FILING DATE: 1999-108-09
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Pred. No. 0.18;
0; Mismatches 71; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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Best Local Similarity 100.0%; Pred. No. 6.4e-49;
Matches 185; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 26:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 209848
LENGTH: 634
                                           TELECOMMUNICATION INFORMATION
                                                                           TELEPHONE: 202-429-0625
TELEFAX: (202) 299-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                         LENGTH: 185 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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52.7%;
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Best Local Similarity 52.7
Matches 79; Conservative
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US-10-027-632-209848/c
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-909-207-26
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                                                                                                            96 AACAGAGAAGGNCTGCATGAAAGGAGGTGATGGGTTTTTTCATCTTAGGGATGACAGAACA 155
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                                                                                                                                                                                                              190 Arcraacaaddaarraaraacrddaararararaacracracracraaraaaaara 131
250 AAAGGATCAACAAATAAACAGATGACCTACAGAACAGGTGATAATATTAGCAATCAACTT 191
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.128
CURRENT APPLICATION NUMBER: US/10/027,632
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Pred. No. 0.18;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 ATACGGATGAAAAAGGAGGGGATGGAAA 185
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                                                                                                                                                                                                                                                                                                                               156 ATACGGATGAAAAAGGAGGGGGGGGATGGAAA 185
                                                                                                                                                                                                                                                                                                                                                                                                                            130 ATTTGATTAAAATGGGTAAAGAATTTGAA 101
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52.7%;
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ORGANISM: Homo sapiens
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US-10-369-493-46834
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Sequence 182736, Application US/10027632

Publication No. US2003020407539

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Tentification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129

CURRENT APPLICATION UNMBER: US 60/218,006

PRIOR PRIOR PLILING DATE: 2000-07-12

PRIOR PELLING DATE: 2000-04-20

PRIOR PELLING DATE: 2000-04-20

PRIOR PELLING DATE: 2000-04-20

PRIOR PELLING DATE: 2000-03-29

PRIOR PELLING DATE: 2000-03-29

PRIOR PELLING DATE: 1909-09-28

PRIOR PELLING DATE: 1999-09-28

PRIOR PELLING DATE: 1999-09-28

PRIOR PELLING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-08

NUMBER OF SEQ ID NOS: 325720

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18.9%; Score 35; DB 1
Best Local Similarity 51.3%; Pred. No. 0.79;
Matches 80; Conservative 0; Mismatches
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PILLING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/199,483
PRIOR PILLING DATE: 2000-03-29
PRIOR PILLING DATE: 2000-03-29
PRIOR PILLING DATE: 2000-03-29
PRIOR PILLING DATE: 1990-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILLING DATE: 1999-11-23
PRIOR PILLING DATE: 1999-10-28
PRIOR PILLING DATE: 1999-09-28
PRIOR PILLING DATE: 1999-09-28
PRIOR PILLING DATE: 1999-09-28
PRIOR PILLING DATE: 1999-09-09
PRIOR FILLING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PRESEED FOR WINDOWS VERSION 4.0
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, ORGANISM: Human
US-10-027-632-182736
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ORGANISM: Human
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Winners S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: BARRESION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(5205)B
CURRENT APPLICATION NUMBER: US/0360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 46834
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                                                                                                                                                      503 ATCAATATGTTTGAATGAGAAGAGCTACCAATAAACCAGAAAGACAAATAGACAGGAAG 444
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DB 15; Length 624;
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APPLICANT: Marc Malandro
TITLE OF INVENTION: NOVEL Therapeutic Targets in Cancer
FILE REPRENCE: 529452001600
CURRENT APPLICATION NUMBER: US/10/388,838
CURRENT FILING DATE: 2003-03-14
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FREISEQ for Windows Version 4.0
SEQ ID NO 84
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                                                                                                                                                                                                                                                                                                                                                                                        383 giragaaartrcacaaaaraaaacaaraaagrga 348
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; Pred. No. 1.3;
0; Mismatches
Score 35; DB :
Pred. No. 0.79
0; Mismatches
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Publication No. US20030233675A1
GENERAL INFORMATION:
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; Publication No. US20040180344A1
; GENERAL INFORMATION:
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Query Match
Best Local Similarity 51.3%;
Matches 80; Conservative
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Best Local Similarity 65.4%;
Matches 51; Conservative
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CRGANISM: Bacillus subtilis
US-10-369-493-46834
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APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 141151
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianteng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE REPRESENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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Pred. No. 3.2;
0; Mismatches 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 CATCTAACAGAGAAGGNCTGCATGAAAGGAGGTGATGGG
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                                                                                                                                                                                                                                                                                            ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_98471C.1
US-10-424-599-141151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 GAACAATACGGATGAAAAAGGAGGGGATGGA 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32.8; DE Pred. No. 7.7; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR FLIMO DATE: 2002-02-21 NUMBER OF SEQ ID NOS: 47374 SEQ ID NO 41036
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Publication No. US20030233675A1
GENERAL INFORMATION:
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59.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Bacillus halodurans
US-10-369-493-41036
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ilarity 51.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 59.1;
Matches 55; Conservative
                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Glycine max
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Best Local Similarity
Matches 76; Conserv
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US-10-369-493-41036
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5323)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                  183682 ATTATGGCTTTCTGGTCTTGGACAACAGGCAGCACAGGAGGAGCAATCACTAAGAGAGT 183623
                                                                                                                                                                                                                                                           183802 CATTGATAATGTTTAGAGCTGCTAAGTTTGTAGCAGTTTGTTATGGCAGCAACAGAAAC 183743
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                                                                                                                                                                                                                                                                                                            62 ATCCATGCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAGAAGGACGTGAAAGGAG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 CAATITCATAATAAAGAAATCATTTATCTAAATACGATTTTGCTTTTATTTGCTTAAAA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 CAGTATCGTTCCATCTAACAGAGGACGACCATGAAAGGAGGTGATGGGTTTTTTCATCT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 CTATTTCATTTGTATCAAAGGATTTATACACAAACAAGAGACATCCATGCCGGGTTAAAG
                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.8%; Score 33; DB 16; Length 445; 50.6%; Pred. No. 3; cive 0; Mismatches 76; Indels
                                                                                                                     Length
                                                                                                               Score 33.2; DB 17;
Pred. No. 35;
0; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: Clone ID: PAT_MRT3847_107339C.1
US-10-424-599-8116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 TAGGGATGACAGACAATACGGATGAAAAAGGA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     retriticiangaaararararaaaararga 92
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Publication No. US20040031072A1
GENERAL INFORMATION:
CTHER INFORMATION: n = A,T,C or US-10-388-838-84
                                                                                                               17.9%;
ilarity 48.6%;
Conservative
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 50.6
Matches 78; Conservative
                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183622 GAA 183620
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                                                                                                                                                           89;
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                                                                                                                                                           Matches
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LOCATION: (372)
OTHER INFORMATION: unsure at all n locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; sequence 4132, Application US/09960352; Patent No. US20020137139A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 23439 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                              309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11601 AAAAAACGAGATG 11614
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ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: unsure
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LENGTH: 405
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Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11481 rargraraaakonerenearenerekrrasooorrekrrekrrekerekriseresresraan 11540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 TATACACAAACAAGACATCCATGCCGGGTTAAAGCAGTATCGTTCCATCTAACAAGA 103
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
TUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32.2; DB 8; Length 23439;
Pred. No. 27;
                                                                                                                                                                                    ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                             ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                           SOFTAMRE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 38, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248
TELECOMMUNICATION INFORMATION:
TELEFAX: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11601 AAAAAACGAGATG 11614
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52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 23439 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 52.23
Matches 70; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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US-10-329-624-38
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MOLECULES ASSOCIATED WITH LACTATION AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11541 ACGACCAAAGAAATTACGAAACGTTTTGTTCAAATTATGGAAGATTAAATGATAACGAT 11600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 TATACACAAACAAGAGACATCCATGCCGGGTTAAAGCAGTATCGTTCCATCTAACAGAGA
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COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
COMPUTER: HP Vectra 486/33
COPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION NUMBER: 08/956,171
PRILING DATE: October 20, 1997
APPLICATION NUMBER: 60/09,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 60/09,861
FILING DATE: January 5, 1997
ATTORNEY/AGENT INPORMATION:
NAME: Mark J. Hyman
REFERENCE/DOCKET NUMBER: 46,789
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: 9248P1D1
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64; Indels
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APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
TITLE OF INVENTION: WUCLEIC ACID AND OTHER MOLECU
TITLE OF INVENTION: MUCLEIC AND FAT DEPOSITION
TITLE OF PREPERRINCE: 16511.066/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
17.4%; Score 32.2; Di
Best Local Similarity 52.2%; Pred. No. 27;
Matches 70; Conservative 0; Mismatches
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Search completed: November 11, 2004, 02:08:31 Job time : 121.282 secs
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                                                                                                                                                                                                                                     122 TATTTCTTTTAAAATAATGTTTTAAAGTTTTTACTACAAAAATCTGGCTTCAACATGGA 63
                                                                                                                                                                                                                                                                                                                                            62 AGCATTTTCCTTTTCAAGATTATACACCTGCATGGAAGAAGGTGATTTCCTTTACATTTA 3
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/199,676
PRIOR APPLICATION NUMBER: US 60/199,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR FILING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-26
PRIOR FILING DATE: 1999-09-09-80-99
PRIOR FILING DATE: 1999-09-09-80-99
PRIOR FILING DATE: 1999-09-09-80-99
PRIOR PLING DATE: 1999-08-09
                                                                                                                                                                                    21 TATTTCATTTGTATCAAAGGATTTATACACAACAAGAGACATCCATGCCGGGTTAAAAGC
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                                                                                    Length 405;
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                                                                                                                                  0; Mismatches 56; Indels
; OTHER INFORMATION: Clone ID: 18-LIB3058-023-Q1-K1-E5
US-09-960-352-4132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.1%; Score 31.6; DB 13;
48.6%; Pred. No. 12;
ive 0; Mismatches 90;
                                                                               Score 32; DB 9;
Pred. No. 6.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 117073, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
                                                                               Query Match
Best Local Similarity 53.7%;
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 48.6
Matches 85, Conservative
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US-10-027-632-117073
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RESULT 15 US-10-027-632-117073/c ; Sequence 117073, Application US/10027632

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915 AAAGCCTCTAAGACTGCCAGTTAGTCATGAATTCAAAGCTAGATGGCTGACCAAAATGA 856
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Dolymorphisms in the Human Genome
FILE SEPERBECE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PAPLICATION NUMBER: US 60/193,483
PRIOR PAPLICATION NUMBER: US 60/195,218
PRIOR APPLICATION NUMBER: US 60/165,363
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-10-24
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-10-09
PRIOR PILING DATE: 1999-10-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GGTGATGGGTTTTTCATCTTAGGGATGACAAAAATACGGATGAAAAAAGGAGA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      855 TATCTGGAAAATGTTTAAAGATTGATACATAGAGAAAGGGATGAAATAAGTATA 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 15; Length 1079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31.6; DB
Pred. No. 12;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 117073
LENGTH: 1079
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48.68;
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Best Local Similarity 48.6
Matches 85; Conservative
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US-10-027-632-117073
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